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Description	Abu07499 Protein d Aae35859 Human HWG Add40789 Human HWG Add40789 Human HWG Add60491 Human hig Ad025918 Human hig Ad071477 Human hig Ad071477 Human hig Ad071477 Human hig Ad071477 Human hig Ad745922 Human hig Ad745922 Human hig Ad745929 Human nmp Ad714248 PRO polyp Ad417645 Human Pro Ad650732 Human Pro Ad650732 Human Pro Ad660732 Human Pro Ad660732 Human Pro Ad660732 Human Pro Ad660732 Human Pro Ad660731 Human Pro Ad617580 Amino aci
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ALIGNMENTS

Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients. Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring. Protein differentially regulated in prostate cancer #102. Claim 1; Page 413-414; 416pp; English. ABU07499 standard; protein; 215 AA (ORIG-) ORIGENE TECHNOLOGIES INC. 08-APR-2002; 2002WO-US010824. 06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P. (first entry) WPI; 2003-058520/05. N-PSDB; ABX10404. WO200281638-A2. Jay G; 28-JAN-2003 Homo sapiens 17-OCT-2002. ABU07499; Sun Z, RESULT 1 $egin{array}{c} egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}$

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer.

motif (HMG1 A box)"

/note= "DNA binding

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CC Preferably, the expression levels of at least 10 genes are determined.

(1) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent under conditions effective for is useful as molecular markers, as drug targets, and for detecting, cataging, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (1) and its expression conditions especially relating to prostate cancer. (2) and its expression conditions especially relating to prostate cancer. (3) and its expression conditions especially relating for expressing the polypeptide encoded by (1) can be used as target for therapy or drug discovery. (1) can also be used for expressing the polypeptide and thus continued as a specific binding partners of the polypeptide and thus continued applications to treat prostate cancer. The identification of the specific genes, and ground to treat prostate cancer. The identification of specific genes, and ground so the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical papelaries of the amino acid sequence of a protein differentially relations of angelence of a protein differentially really and a procession of a protein differentially really and a procession and sequence of a protein differentially really and a procession and a protein differentially really and a procession and sequence of a protein differentially really and and a procession and a protein differentially and and a procession and a protein and a procession and a procession of a protein differentially and and a procession and a procession and a procession and a procession and a proc
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Location/Qualifiers

Binding-site

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New isolated polypeptide having a vertebrate HMG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetee
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/note= "DNA binding motif (HMG1 B box)"
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This invention describes a novel method comprising using high mobility group B proteins (HMGB) as target molecules for development or preparation of compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention are used in kit for characterising the status of the endometrium, especially for presence of pregnancy or irregularities in the menstrual cycle. The proteins used in the invention can be HMGB! 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor for advanced glycation end products). The products of the invention have gynaecological, contraceptive and cytostatic activity. HMGB is part of a nuclear transcription factor complex and, extracellularly, a ligand for the surface RAGE (receptor for advanced glycation end products) which is involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometrions or diagnoses of endometrial disease, particularly particularly for detecting pregnancy or menstrual disease. This sequence represents the human HMGB1 protein used in the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Developing treatment and diagnosis of endometrial disorders, using high mobility group B proteins, or related nucleic acid or interaction partners, as targets.
                                                       high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease, contraceptive; endometrium; pregnancy; menstrual cycle irregularity; RAGE; receptor for advanced glycation end; gynaecological; cytostatic; nuclear transcription factor complex; tumour metastasis; endometriosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 43pp; German.
                                                                                                                                              polyps; hyperplasia; carcinoma.
                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2001; 2001DE-01062556.
                                                                                                                                                                                                                                                                                                                       19-DEC-2002; 2002WO-EP014579.
                                                                                                                                                                                                                                                                                                                                                                                                          (ALCE-) ALCEDO BIOTECH GMBH
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Best Local Similarity 100.
Matches 215; Conservative
                    Human HMGB1 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-505462/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bullerdiek J;
                                                                                                                                                                                             Homo sapiens.
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This invention describes a novel method comprising using high mobility group B proteins (HMGB) as target molecules for development or group B proteins (EMGB) as target molecules for development or compositions (compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention or especially for presence of pregnancy or irregularities in the menstrual cycle. The proteins used in the invention partner for HMGB1, 2 or 3, or SP100-CC HMG, and the preferred interaction partner for HMGB1, 2 or 3, or SP100-CC HMG, and the preferred interaction partner for HMGB1, 2 or 3, or SP100-CC FMG, and the preferred in the invention named of the invention have gynaecological, contraceptive and cytostatic activity. HMGB is part of a nuclear transcription factor complex and, extracellularly, a ligand for the surface RAGE (receptor for advanced glycation end products of the invention are used to involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometrious and methods for assessing status of the endometrium, also contraceptives and methods for assessing status of the condensitium, particularly for detecting pregnancy or menstrual disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;
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                                                                                                                                                                                contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
nuclear transcription factor complex; tumour metastasis; endometriosis;
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100.0%; Pred. No. 2.7e-93;
iive 0; Mismatches 0;
ADD40788 standard; protein; 215 AA.
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                                                                                                                                                                                                                                          polyps; hyperplasia; carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2001; 2001DE-01062556
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N-PSDB; ADD40787.
                                                                                                                     Human HMGB1 protein.
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ses 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bullerdiek J;
                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                               15-JAN-2004
                                       ADD40788;
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N-PSDB; ADO60490
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                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                   ADO60491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are associated with carcinomas. The sequences are useful for: (i) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (ivi) for treating carcinoma; (viii) for neutralizing the activity of CAP; (ivi) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ivi) for determing carcinoma are neutralized (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CAP. Note: This patent is an equivalent to basic patent US2002182586AI, for which no sequence data was published
SIGDVAKKIGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
           EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to novel DNA and protein sequences which
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100.0%; Pred. No. 2.7e-93;
ive 0; Mismatches 0;
                                               215
                                                                                                                                                                                                                              Cytostatic; carcinoma; lymphoma; cancer; human.
                                               SKKKKEEEEDEEDEEDEEDEEDEDEEEDDDDE
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                                                                                                                                ABM85677 standard; protein; 215 AA
                                                                                                                                                                                                       Human protein sequence hCP43793.
                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                                           28-FEB-2003; 2003WO-US006235
                                                                                                                                                                               (first entry)
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Matches 215; Conservative
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                                                                                                                                                                                                                                                                            WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 215 AA;
                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                    12-SEP-2003.
                                                                                                                                                                              18-NOV-2004
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This invention relates to a novel vaccine for promoting amyloid beta 42 aggregation inhibitory effect and/or amyloid beta 42 phagocytesis by microglia, which comprises a high mobility group protein 1 (HMGI), its partial peptide, or its salt. The invention may be useful for the production of compounds with a nootropic or neuroprotective activity acting a promoters of inhibition of amyloid beta 42 aggregation or promoters of amyloid beta 42 phagocytosis by microglia. The invention may also be useful for the production of a vaccine. The invention is useful for prophylaxis and/or treatment of Down's syndrome or amyloid angiopathy or preventing brain amyloidosis such as Alzheimer's disease. The present sequence is that of the protein encoded by the human high mobility group protein 1 (HMGI) gene which may be used during the creation of the novel
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vaccine; amyloid beta 42 aggregation; amyloid beta 42 phagocytosis; microglia; high mobility group protein 1; HMG1; nootropic; neuroprotective; microglia; vaccine; Down's syndrome; amyloid angiopathy; brain amyloidosis; Alzheimer's disease; human.
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100.0%; Pred. No. 2.7e-93;
ive 0; Mismatches 0;
                                                                                                                                                                    SKKKKEBEEDBEDGEDEEEEBDEEDEEDDDDE 215
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Matches 215; Conservative
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The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual. The composition individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) that can be used to stimulate cytokine activity and increase immune response to assist in treating disease.
SIGDVAKKIGEMMINITAADDKQPYEKKAAKIKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pharmaceutical composition comprises a polypeptide comprising an HMGB box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.
                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; vaccine; pharmaceutical composition; HMGB B box; high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1149; DB 8; Length 215; 100.0%; Pred. No. 2.7e-93; ive 0; Mismatches 0; Indels 0
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                                                                                               SKKKKBEEEDEEDEEDEEDEEDEEDEEDEEDDDE 215
                                                                            SKKKKEBEEDEEDEEDEEEEEDEEDEDEEEDDDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES
                                                                                                                                                                                                                                                                                                                     Human high mobility group box 1 (HMG1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1; 68pp; English.
                                                                                                                                                                                                         AD025918 standard; protein; 215 AA
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                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
Matches 215; Conservative
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B conspitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for effecting whether a compound inhibits inflammation, a pharmaceutical determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an artibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an useful in treating obesity and conditions characterised by activation of an each of the condition and methods are useful in treating obesity and conditions characterised by activation of
                   Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; chronic is particulis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
SIGDVAKKIGEMMNNTAADDKQPYEKKAAKIKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
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                                                                                                                                                                                                                                                                                                                                                                                                   Human high mobility group box 1 (HMGB1) protein #1.
                                                                                                                       SKKKKEEEEDEEDEEDEEEEDEBDEE 215
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                                                                                                                                                                                                                                                          ADO71477 standard; protein; 215
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1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL

MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF

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degeneration, arthritis, endometriosis, histiocytosis, psoriasis, rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma, Kaposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis, angina pectoris, ischaemia, infarction, interility, wounds (including diabetic and other ulcers), also diseases associated with DNA damage, especially xeroderma pigmentosum, 'leather skin', skin cancers and ageing (including where associated with sunburn) and cardiac infarct, including cosmetic treatment, especially as a sun-protection composition. Compounds identified as modulators of the specified processes can also be used therapeutically. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDMAKADKARYEREMKTYIPPKGETKKKKKDNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; badder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated antigenic target (TAT) polypeptide PRO71096, SEQ:3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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   (proliferative) diabetic retinopathy, diabetic nephropathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1149; DB 8; ilarity 100.0%; Pred. No. 2.7e-93; Conservative 0; Mismatches 0;
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Matches 215; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 215 AA;
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human.
                                                                                                                                                                                                                                                                                                                                                                                                           EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                   EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
                                                                                                                                                                                                                                                                        1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKBKGKF
                                                                                                                                                                                                         Gaps
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                                                                                                                                      Length 215;
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                                                                                                                                                                                                         Indels
represents a human HMGB1 polypeptide of the invention
                                                                                                                                      100.0%; Score 1149; DB 8; 100.0%; Pred. No. 2.7e-93;
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                                                                                                                                                                                                     0; Mismatches
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07-MAR-2003; 2003DE-010160.
10-AUG-2003; 2003DE-0105642.
08-OCT-2003; 2003DE-01046614.
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                                                                                                                    Query Match
Best Local Similarity 100.
Matches 215; Conservative
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                                                                   Sequence 215 AA;
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide equences at least 80% identical to the TAT nucleic acids and polypeptide and polypeptide and polypeptide and polypeptide and polypeptide and enthode and compositions for the treatment or TAT polypeptide; and methods and compositions for the treatment or TAT polypeptide, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosis of cancer in mammals. TAT polypeptides and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cervical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, inverse system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome addentification and in gene therapy. The present sequence represents a TAT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor; VEGF; VEGFR; dermatological; vascular endothelial growth factor receptor; VEGFR; dermatological; edema; gene therapy; vulnerary; injury; burn; skin cancer; cytostatic; wound healing; hematoma; pain; necrosis; ischemia; vasotropic; anglogenesis stimulation; vascularization; tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTWSAKEKGKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                     Claim 12; SEQ ID NO 3888; 7273pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADW81011 standard; protein; 215 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 215; Conservative
  prostate cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005011722-A2.
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The present invention relates to new vascular endothelial growth factor (VEGF) proteins useful for skin healing of a skin graft onto underlying tissue. The method involves contacting a skin graft flap or underlying tissue with an agent chosen from vascular endothelial growth factor C (VEGF-C) polymucleotides, vEGF-C polympetides, VEGF-D polymucleotides, or amount effective to reduce edema or increase perfusion at skin graft or flap. The composition comprises a gene therapy vector that encodes VEGF-C polymotleotide. The VEGF-C polympetides agene therapy vector that encodes VEGF-C polymotleotide. The VEGF-C polympetides agene therapy vector that encodes VEGF-C polymotleotides. The VEGF-C polympetides are preparational X-B-Z or Z-B-X, where X binds VEGF-3, where Z comprises a heparin-binding amino acid sequence, and B comprises a performent linking X to Z. The VEGF-D polympetides, VEGF-D polymotleotides, and WEGF-D polympetides, VEGF-D polymotleotides, and WEGF-D polympetides, vEGF-C polymotleotides, vEGF-C polymotleotides, vEGF-C polympetides, VEGF-D polymotleotides, and NEGF-D polympetides or vEGF-C polymotleotides with susful in treating skin injury such as burns or skin cancer, skin grafts, cosmetic surgery, a liposuction procedure, or in reconstructive surgery. The subject is disbetic. The method is useful for improving post-surgical wound healing after reconstructive and cosmetic surgery and improves complications resulting comprised wound-healing difficulties, pain, edema, necrosis and behavising and wound-healing difficulties, pain, edema, necrosis and cischemia. The present sequence is amphoterin protein, which contains a heparin binding domain related to the invention.
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                                                                                                                                                                                                                                           Improving healing of skin graft or skin flap to underlying tissue useful in mastopexy, cosmetic surgery, abdominoplasty, involves using composition of vascular endothelial growth factor-C or D polynucleotides
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                                                                                                                                 Tammela T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1149; DB 9; 100.0%; Pred. No. 2.7e-93;
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                                                                                                                                                                                                                                                                                                                                                          Example 11; SEQ ID NO 22; 119pp; English.
                                                                                                                                 Karkkainen M,
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                                                                (LUDW-) LUDWIG INST CANCER RES
                         12-JUN-2003; 2003US-0478390P.
12-JUN-2003; 2003US-0478114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 215; Conservative
                                                                                                                                 Alitalo K, Saaristo A,
Yla-Herttuala S, He Y;
                                                                                     (LICN ) LICENTIA LTD
                                                                                                                                                                                               WPI; 2005-142834/15.
                                                                                                                                                                                                                                                                                                                 and/or polypeptides
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ADY85326 standard; protein; 215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to heparin-binding vascular endothelial growth factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The heparin binding VEGFR-3) proteins are used for stimulating lymphangiogenesis or angiogenesis in a mammal, and for modulating the growth of mammalian endothelial cells, mammalian endothelial precursor cells or hematopoietic progenitor cells. The polypeptide may also be used for promoting recruitment, proliferation, differentiation, migration or survival of neuronal cells or neuronal precursor cells, and for treating neurodegenerative disorder, e.g. Alzheimer's diseases, Parkinson's disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral Sclerosis (ALS), dementia, or cerebral palsy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                    amphoterin; Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian; Anticonvulsant; VEGF-3 receptor; Angiogenesis stimulator; Gene Therapy; vascular endothelial growth factor receptor 3; VEGFR-3; angiogenesis disorder; neurodegenerative disorder; Alzheimers disease; Parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C; neurological disease; Huntingtons chorea; vascular endothelial growth factor receptor 3; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 63; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                         12-JUN-2003; 2003US-0478390P.
23-SEP-2003; 2003US-00669176.
                                                                                                                                                                                                                                                                                                                                                                                            Tammela T;
                                                                                                                                                                                                                                                                                            .2-JUN-2003; 2003US-0478114P.
                                                                                                                                                                                                                                                                 14-JUN-2004; 2004WO-US019122
(first entry)
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les 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-182331/19.
                                                                                                                                                                                                                                                                                                                                                                                          Alitalo K, He Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 215 AA;
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                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatcid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
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                                                                                                                                                                                                Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
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                                                                                                                                                                                                                       Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Heparotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; diagnosis.
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; Pred. No. 2.7e-93;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 54; 158pp; English
ADY14248 standard; protein; 215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 215; Conservative 0
                                                                                                                                                 PRO polypeptide SEQ ID NO 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2004; 2004WO-US026249.
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                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     WO2005016962-A2.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide.
                                                                                                05-MAY-2005
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                                              ADY14248;
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High mobility group box; HMGB1; immune disorder; infection; immunosuppressive; autoimmune disease; allergy; antiallergic; ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; asthmatic; rheunation; asthma; antiathritis; antirheunatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
                                   Human high mobility group box protein HMGB1.
                                                                                                                                                                                                                              (GEHO ) GEN HOSPITAL CORP.
(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES
                                                                                                                     Location/Qualifiers
                                                                                                                             32. 85
/label= A_box
                                                                                                                                                    /label= B_box
                                                                                                                                                                                                  10-SEP-2004; 2004WO-US029540.
                                                                                                                                                                                                                10-SEP-2003; 2003US-0502349P
                      (first entry)
                                                                                                                                              .161
                                                                                                                                                                                                                                                     Warren HS, Tracey KJ;
                                                                                                                                                                                                                                                                   WPI; 2005-233421/24.
                                                                                                                                                                   WO2005025604-A2
                                                                                                        Homo sapiens
                      02-JUN-2005
                                                                                                                                                                                   24-MAR-2005
       ADY85326
                                                                                                                              Region
                                                                                                                                              Region
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Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment

Claim 6; SEQ ID NO 1; 57pp; English.

The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural HMGB A box. The immune pathology is induced by the administration of a non-human antigen, nonself material (e.g. a cell or tissue such as bone marrow cells) or sallwart to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune response to an immunosuppressive fragment of decreasing an immune response to an immunosuppressive fragment of the vertebrate or non-natural A box, or an immunosuppressive fragment of the vertebrate or non-natural A box, or an immunosuppressive fragment of the vertebrate or non-natural A box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural A box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural A box. Comprises administering a vertebrate or non-naturally-occurring HMGB A box, or an immunosuppressive fragment of these, and a vertebrate or non-naturally box. Comprises administering a vertebrate or non-naturally box. The HMGB polypeptide is preferably a HMGB polypeptide and may be truncated at the C-terminus. The autoimmune disease is allergy, culterative collits, Crohn's disease, asthma, rheumacoid arthritis, percent or sequence is that of the human HMGB protechin, which can be used as the cell HMGB polypeptide in methods of the invention.

Sequence 215 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High mobility group box; HMGB1; monoclonal antibody; antibody therapy; sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antiantinitial antianthmitic; lupus erythematosus; antiantialmantory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                                                             61 EDMAKADKARYEREMKTY1PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
                                                                                 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                         SIGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
                                                           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNPSEPSKKCSERWKTMSAKEKGKF
                                                                                                                            EDMAKADKARYEREMKTY1 PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPK1 KGEHPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease;
                                 Gaps
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 Length 215;
                               Indela
 DB 9;
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                                                                                                                                                                                                                                                                                        SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
Score 1149; DB 9;
Pred. No. 2.7e-93;
; Mismatches 0;
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100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human HMGB1 A box.
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detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB A box but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB protein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, peniconitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cacheria, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGBI ADY85012. An identical
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Matches 215, Conservative
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Search completed: April 6, 2006, 10:19:12 Job time : 263.97 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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OM protein - protein search, using sw model

April ë Run

6, 2006, 10:19:38 ; Search time 41.0197 Seconds (without alignments) 504.309 Million cell updates/sec

US-10-717-984-1 1149

1 MGKGDPKKPRGKMSSYAFFV......DEEBEBDBBDBBBBDDDB Perfect score: Sequence:

215

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	stone christone	high mobility grou
SUMMARIES		
SUMM. ID	\$02826 \$020826 \$020824 \$020827 \$02355 \$02355 \$02355 \$02355 \$021114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$011114 \$0114 \$0114 \$01114 \$	T03640
DB	0110000000000000000000000000000000000	0
Length	215 215 215 215 216 216 217 210 210 200 200 200 200 200 200 200 200	168
\$ Query Match	$\begin{array}{c} 0.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0$	27.1
Score	1145 11145 11145 11140 11122140 9 2 6 4 5 5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	311
Result No.	11111111111111111111111111111111111111	29

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Gaps

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Indels

9

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61

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121

g 8

SKKKKEEEEDEEDEEDEEEEDEEDEDEEDEDDDE 215

181

1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF

high mobility grou HMG protein [impor	nign mobility grou embryogenic callus HMG1 protein homol	high mobility grouhigh mobility grouhigh mobility grou	high mobility grou DNA-binding protei	high mobility grouhigh mobility grou	<pre>structure-specific hypothetical prote high mobility grou</pre>
B47150 T51159	S18991 T14286 S68823	109301 S39556 S40302	T02252 A41265 S40122	S78050 S35637	A41976 T08187 T51597
000	2000	100	000	0 10	000
157	502	149	142 708 154	669 561	709 446 144
27.0	23.5 23.5 23.6	23.3	22.9 22.6 52.6	22.2	21.8 21.8 21.7
310	288.5 278.5 271	267.5 264	263.5 259.5 259	255.5	251 250 249.5
30	3 65 67 2 65 47	36	38 39 40	4 4 2	4 4 4 5 4 5

ALIGNMENTS

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C;Species: Homo sapiens [man]
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
R;Wen, L; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
                                                                                                                                                                                                                                                                                                                 A;Accession: S02826
A;Molecule type: mRNA
A;Residues: 1-215 <WENA
A;Residues: 1-215 <WENA
A;Cross-references: UNIPROT: P09429; UNIPARC: UDI0000015ED; EMBL: X12597; NID: G32326; PIDN
B;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro
A;Reference number: A33178; MUID: 91176935; PMID: 2079031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:133789; OMIM:163905
A; Map position: 13q12-13q12
C; Superfamily: norhistone chromosomal protein HMG-2; HMG box homology C; Keywords: chromosomal protein; DNA binding; nucleus F; 6-83/Domain: HMG box homology < HMG1>
F; 92-166/Domain: HMG box homology < HMG2>
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nonhistone chromosomal protein HMG-1 - human
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A;Mesidues: 2-13, XXF' <WAR>
A;Cross-references: UNIPARC:UPI00001771D7
A;Accession: G33178
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A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UP100001771D7
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us-10-717-984-1.rpr

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N;Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A41175; A27298; A30188; B48771; A48771; C48771
R;Merenmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
A;Hitle: 30-kba heparin-binding protein of brain (amphoterin) involved in neurite outgrov
A;Reference number: A41175; MUID:91158468; PMID:1885601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN:PA;Note: part of this sequence, including the amino end of the mature protein, was confirm A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-10, R'. 12-82,84-95,97,'AS',100-215 <PAO>
A; Cross-references: UNIPARC:UP10000173984
R; Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.
J. Cell Biol. 107, 2293-2305, 1988
A; Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
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R, Paonessa, G.; Frank, R.; Cortese, R.

Nucleic Acids Res. 15, 9077, 1987

A, Title: Nucleotide sequence of rat liver HMG1 cDNA.

A, Reference number: A27298; MUID:88067717; PMID:3684582

A, Accession: A27298
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                nonhistone chromosomal protein HMG-1 - rat
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F;92-166/Domain: HMG box homology <HMG2>
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Best Local Similarity 99.1
Matches 213; Conservative
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A, Molecule type: mRNA
A, Residues: 1-215 <MER>
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: 30-Sep-1989 #sequence revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; Acifoli; S10959; 145910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length CDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
A;Molecule type: mRNA
A;Residues: 1-215 «KAP>
A;Ccession: S01947
A;Molecule type: mRNA
A;Residues: J.Z. 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: Acidil; MUID:81138848; PMID:7202717
A;Reference number: Acidil; MUID:81138848; PMID:7202717
A;Recession: Acidil
A;Molecule type: protein
A;Residues: 2-22, 'S',2440;48-105,'A',107-157,'X',160-193,'D',195 «WAL>
A;Residues: 2-22,'S',2440;48-105,'A',107-157,'X',160-193,'D',195 *WAL>
A;Cross-references: UNIPARC:UPI0000173998
B;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FEBS Lett. 267, 139-141, 1990
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A.Fattle: High mobility group proteins 1 and 2 bind preferentially to brominated poly (dd-A; Reference number: S10726; MUID: 90306387; PMID: 2365081

A.Accession: S10959

A.Molecule type: protein
A; Residues: 2-22, 'X', 24-38 «CHR»
A; Cross-references: UNIPARC: UPI0000173989

R; Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A; Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-grout A; Reference number: 145910; MUID: 84128872; PMID: 6141822
A; Reference number: 145910; MUID: 84128872; PMID: 6141822
A; Recession: 145910
A; Return Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 'PGG', 119, 'V', 121-215 «PEN»
A; Residues: 'PGG', 119, 'V', 121-215 (PEN»
A; Residues: 'PGG', 'INPARC: 'PGG', '
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181 SKKKKEEEEDEEDEEDEEEEEDEEEEEDDDDE 215
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nonhistone chromosomal protein HMG-1 - bovine
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A;Molecule type: DNA A;Residues: 1-216 <2TN.
A;Residues: 1-216 <2TN.
A;Residues: 1-216 <2TN.
A;Cross-treferences: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
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C,Species: Xenopus laevis (African clawed frog)
C,Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
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R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: $29857; MUID:93176821; PMID:8439568
A;Accession: $29857
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DNA binding; nucleus F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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Pred. No. 3.5e-60;
0; Mismatches 2; Indels 1;
                                                                                                                                                                                    Length 215;
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                                                                                                                                                                                    99.2%; Score 1140; DB 2;
99.1%; Pred. No. 3.2e-61;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonhistone chromosomal protein HMG-1 - human
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F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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98.6%;
                                                                                                                                                                                                                          llarity 99.1%;
Conservative
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Best Local Similarity 98.6
Matches 213; Conservative
                                                                                                                                                                                                                      Best Local Similarity
Matches 213; Conserv
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nonhistone chromosomal protein HMG-1 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: A28897

C;Accession: A28897

B;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.

Biochemistry 27, 6159-6163, 138

A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequent

A;Reference number: A28897; MUID:89050965; PMID:3191113

A;Accession: A28897

A;Accession: A28897

A;Accession: A28897

A;Accession: C;Coss. C;Co
                                                                                                                                                                                                                          A;Title: Nuclectide sequence of a mouse cDNA encoding the nonhistone chromosomal high md A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Accession: I48688
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Molecule type: mRNA
A; Reaidues: 1-215 < RES>
A; Cross-references: UNIPROT:P07155; UNIPARC; UP100000008A6; EMBL:Z11997; NID:g53381; PIDN
R; Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
A; Eiol. Chem. 269; 28803-28808, 1994
A; Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A; Reference number: A55402; MUID:95050689; PMID:7961836
A; Accession: A55402
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Mamm. Ganome 5, 91-99; 1994
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse A;Reference number: 157021; MUID:94235965; PMID:8180479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; C;Genetics:
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   non-histone chromosomal high-mobility group 1 protein - mouse C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 146688; A55402; T57021
R;Yotov, W.V.; &L-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
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Pred. No. 2.4e-61;
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A;Residues: 1-189,'E',191-215 <FER>
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Best Local Similarity 99.1
Matches 213; Conservative
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high mobility group 2 protein - mouse close who musculus (house mouse) CjSpecies: Mus musculus (house mouse) CjSpecies: Mus musculus (house mouse) CjSpecies: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 CjAccession: S54774; S52211 Wirth, T. EMBO J. 14, 1198-1208, 1995 A;Title: High mobility group protein 2 functionally interacts with the POU domains of oct. A,Reference number: S54774; MUID:95237201; PMID:7720710 A,Recession: S54774 A,Status: preliminary; nucleic acid sequence not shown
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A;Residues: 1-210 <ZWI>
A;Cross-references: UNIPROT:P30681; UNIPARC:UP1000016432C; EMBL:Z46757; NID:g609168; PIDN
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
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NSHUH2

NORHUR2

NORHUR2

NORHUR2

NORHUR2

NORHUR2

NORHUR3

C, Species: Homo sapiens (man)

C, Species: Homo sapiens (man)

C, Species: Homo sapiens (man)

C, Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C, Alle S, S20066; S18068

R, Shirakawa, H.; Yoshida, M.

J. Biol. Chem. 267, 6641-6645, 1992

A, Feference under: A42425; MUID:92202209; PMID:1551873

A, Reference number: A42425

A, Molecule type: DMA

A, Residues: 2-209 cSHI>
A, Ross-references: UNIPROT:P26583; UNIPARC:UP1000012CA25; GB:M83665; NID:9184235; PIDN:
A, Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)

A, Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)

A, Note: initiator Mer not shown

R, Majundar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M Nucleic Acids Res. 19, 6643, 1991

A, Title: Sequence of human HMG2 cDNA.

A, Reference number: S20061; MUID:92093633; PMID:1754403

A, Accession: S20061

A, Molecule type: mRNA

A; Residues: 1-209 cMAJ>
A; Cross-references: UNIPARC:UPI000013834D; EMBL:X62534; NID:932332; PIDN:CAA44395.1; PID

C, Genetics:
A, Archiver Sequence of Color of Numan HMG2 cDNA.
A, Residues: 1-209 cMAJ>
A, Cross-references: UNIPARC:UPI000013834D; EMBL:X62534; NID:932332; PIDN:CAA44395.1; PID
C; Accession: S62355
R;Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
BMBO J. 15, 548-561, 1996
A;Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in A;Reference number: S62355, MUID:96174815; PMID:8599938
A;Accession: S62355
A;Accession: S62
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.7%; Score 984.5; DB 2; Best Local Similarity 83.7%; Pred. No. 5.3e-52; Matches 180; Conservative 20; Mismatches 10.
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C,Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Bischemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nuclec A;Reference number: A34719; MUID:90275208; PMID:2350545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:A;Cs:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology chwGing; nucleus
F;6-83/Domain: HMG box homology chwGin
F;92-166/Domain: HMG box homology cHMGi>
                                                                                                                            EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                            121 SIGDVAKKUGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonhistone chromosomal protein HMG-2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKAPDSSVNFAEFSKKCSERWKTMSAKEKSKF
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A;Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A;Reference number: JC1129; MUID:92290291; PMID:1601311
A;Accession: JC1129
A;Accession: JC1129
A;Accession: JC1129
A;Accession: JC1729
A;Residues: 1-207 <SSPA
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171348; GB:M80574; NID:g211928; PIDN: C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG2>
F;92-166/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession. A27853 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
R;Leb. K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Reference number: A27853; MUD:87259986; PMID:3601666
A;Accession: A27853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CSEYRPKIKGEHPGLSIGDVAKKLGEMWANTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 120
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A; Residudes: 1-170 <LEE>
A; Cross-references: UNIPROT: P07156; UNIPARC: UP100001771D5
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords: chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <AHMG2>
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                                                                                                                                                                                                                                                                                                                                                                                      2; Length 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Score 905; DB 2;
Pred. No. 2.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
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high-mobility-group-1 protein - trout
                                                                                                                                                                                                                                                                                                                                                                                      78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                 80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.8<sup>1</sup>
Matches 168; Conservative
   R; Sparrow, D.B.; Wells, J.R.E.
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                 Gene 114, 289-290, 1992
A; Title: Sequence of a c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high-mobility group protein 2 - chicken
Cispeciaes Gallus gallus (chicken)
Cispeciaes Gallus gallus (chicken)
Cispeciaes Gallus gallus (chicken)
Cibate: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 09-Jul-2004
Cisate: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 09-Jul-2004
Ciscession: JC1114
Ribavis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt
A;Reference number: JC1114; MUID:92241676; PMID:1572546
A;Residues: 1-207 cDAV>
A;Residues: 1-207 cDAV>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171347; GB:MB3235; NID:g211926; PIDN:
C;Comment: The high mobility group proteins are among the most abundant nonhistone chromosomal protein HMG-2; HMG box homology
C;Reywords: DNA binding; mucleus
F;G-03/Domain: HMG box homology cHMG1>
C;Cyperfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Reywords: DNA binding; mucleus
F;G-03/Domain: HMG box homology cHMG1>
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                                                                                                                                                                                                                                                                                          1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNPAEFSKKCSERWKTMSAKEKSKF 60
                                                                                                                                                                                                                                          1 MGKGDPKKPRGKMSSYAFFVOTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                                      Length 210;
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81.2%; Pred. No. 7e-48;
ive 17; Mismatches 22; Indels
                                                                                                                                                                             21; Indels
                                                                                                                Query Match

80.0%; Score 919; DB 2;
Best Local Similarity 80.5%; Pred. No. 4.1e-48;
Matches 169; Conservative 20; Mismatches 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKKKAEPEEEEEEEDEEEEEEEEE 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;92-166/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 81.2% Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                          61
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6, 2006, 10:26:18

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Search completed: April Job time: 42.0197 secs
                                                 염
C;Species: Salmo sp. (trout)
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708 #sequence and structure of a gene encoding trout testis high-mobility-group
A;Ritle: cDNA sequence and structure of a gene encoding trout testis high-mobility-group
A;Reference number: S48708 #WID:95045507; PMID:7957172
A;Accession: S48708
A;Reference number: S48708
A;Residues: 1-204 eSTR>
A;Cross-references: UNIPRAC:UPI0001771D9
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;3-82/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Night mobility group protein T - rainbow trout
NyAlternate names: HMG-T protein
Cispecies: Oncortynchus mykiss (rainbow trout)
Cispecies: Oncortynchus mykiss (rainbow trout)
Cispecies: Oncortynchus mykiss (rainbow trout)
Ciste: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
Ciste: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
Cistecssion: T01071
Ripentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1988
Aitle: Isolation and sequence of CDNA clones coding for a member of the family of high Aitle: Isolation and sequence of CDNA clones coding for a member of the family of high Aitle ence number: A24019; WUID:85269614; PMID:402777
Aixelession: T01071
Aixelession: T1-204 FERNA
Aixelidus: L1-204 FERNA
Aixelidus: L1-204 FERNA
Aixelidus: UNIPROT:P07746; UNIPRAC:UPIO00012CA3B; EMBL:X02666; NID:g64327; PIDN Cisuperfemily: nonhistone chromosomal protein HMG-2; HMG box homology
F;91-165/Domain: HMG box homology <HMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SIGDVAKKLGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.9%; Score 837.5; DB 2; Length Best Local Similarity 71.8%; Pred. No. 2.8e-43; Matches 150; Conservative 34; Mismatches 20; Indels
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 6, 2006, 10:13:48; Search time 253.898 Seconds (without alignments) 597.439 Million cell updates/sec Run on:

US-10-717-984-1 1149 1 MGKGDPKKPRGKMSSYAFFV......DEBEBEDBEBDEDBEBDDDB 215 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 Total number of hits satisfying chosen parameters: 2166443 seqs, 705528306 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23		Description	N Q5t7c3 homo sapien	Q4r844	H Q9qx40 spalax leuc	Q6yka4	P09429	Q9qwy6	Q548r9		P10103	088611	088612	P63158		E Qép202 mus musculu			Q8bq02	99yh <u>0</u> 6	Ogpuk9	Q9ngj4 homo	Omod 9vgu60	Q5t7c5 homo	Q6p4n5 xenop		Q5bkq1			Omud80		P07156 מנולווזפטליזס
SUMMARIES		ΩI	QST7C3 HUMAN	Q4R844 MACF	Q9QX40_SPAEH	HMG1 CANFA	HMG1 HUMAN	Q9QWY6 SPAEH	Q548R9 RAT	Q58EV5_MOUS	HMG1 BOVIN	088611 SPAEH	088612_SPAEH	HMG1 MOUSE	HMG1_RAT	Q6P202 MOUS	HMG1 PIG	Q14321 HUMAN	Q8BQ02 MOUS	O9YHO6 CHIC	Q9PUK9 CHIC	Q9NQJ4 HUMA	HMG1X HUMAN	QST7CS_HUMA	Q6P4NS_XENT	Q7SZ42 XENL	Q5BKQ1 MOUS	Q91596 XENLA	Q6GNQ5 XENLA	Q8BNM0 MOUSE	Q8C7C4 MOUSE	HMG1 CRIGR
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		Length	215	215	215	214	214	215	215	215	214	215	215	214	214	215	214	215	215	215	214	211	211	192	211	211	206	210	210	181	178	Cac
,	* Query	Match	100.0	100.0	99.7	99.6	9.66	99.4	99.4		99.2	99.1	0.66	99.0	99.0	98.9	98.8	98.3	97.9	92.9	92.4	92.3	91.4	89.2	87.5	87.1	86.7	85.7	85.4	84.3	83.1	c C
		Score	1149	1149	1145	1144	1144	1142	1142	1142	1140	1139	1138	1137	1137	1136	1135	1129	1125	1067	1061.5	1061	1050.5	1025	1005	1001	966	984.5	981.5	696	955	O V O
	Result	Ñ.	1	7	c	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	26	27	28	29	30

RESULT 2
Q4R844_MACFA
ID Q4R844 MACFA PRELIMINARY; PRT; 215 AA.
AC Q4R844_DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annocation update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annocation update)
DT 15-SEP-2005 (TEMBLrel. 31, Last annocation update)
DF Testis CDNA clone: QtsA-13487, similar to human high-mobility group

4 N N N N N N N N N N N N N N N N N N N	208 1 HMG2 HUMAN P26583 homo sapien 209 1 HMG2_PIG P17741 sus scrofa 208 2 Q5F0P071 HUMAN Q5u071 homo sapien 210 2 G5FVP0_RAT P30681 mus musculu 209 1 HMG2_RAT P526584 gallus morv 209 1 HMG2_RAT P26584 gallus gall 210 1 HMG2_RAT P26584 gallus gall 211 2 Q8AV03 XENICA Q8av03 xenopus lae 212 2 QAVVA XENILA Q75xm1 homo sapien 212 2 Q7ZXK5 XENILA Q72xK5 xenopus lae 212 2 Q6F7M9 XENIR Q6F7M9 xenopus lae 212 2 Q6F7M3 XENIR Q6F7M9 xenopus lae 212 2 Q6F7M5 XENIR Q6F7M9 xenopus lae 212 2 Q6F7M5 XENIR Q6F7M9 xenopus lae 212 2 Q91764 XENIRA Q91764 xenopus lae	ALIGNMENTS 29, Created) 29, Last sequence update) 1-550P23.1-004; data; Craniata; Vertebrata; Euteleo chontoglires; Primates; Catarrhini; Chontoglires; Primates; Catarrhini; Fin; IEA. 1.1, -1, Genomic_DNA. 1.1, -1, Genomic_DNA. 1.1, -1, Genomic_DNA. 1.1, -1, Genomic_DNA. 1.2, -1, Genomic_DNA. 1.3, -1, Genomic_DNA. 1.4, -1, Genomic_DNA. 1.5, -1, Genomic_DNA. 1.6, -1, Genomic_DNA. 1.7, -1, Genomic_DNA. 1.8, 1EA. 1.9, 1EA.	imilarity 100.0%; Score 1149; DB 2; Length 215; 100.0%; Pred. No. 6.9e-59; Indels 0; Gaps 0; CORSETVATIVE 0; Mismatches 0; Indels 0; Gaps 0; MGKGDPKKPRGKMSSYAFFVQTCREEHKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
924 921.5 921.5 921.5 921.5 912.5 912.5 912.5 893.5 884.	2.08 11 2008 1	PRELIMINARY (TTEMBLrel. (TTEMBLrel. (TTEMBLrel.) Group box (MrNames-RPl (Trent)	100.0%; Conservative Conservative COPEKKPRGKMSSYAFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee K.-L.D., Lum H.-K., Nevo E.;
L. Submitted (AUG1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR078820; AAC27653.2; -; Genomic_DNA.
R. HSSP; P07156; 1MRN.
R. SMR; O90X40; 2-84, 93-171.
R. GO; GO:0000785; C:chromatin; IEA.
R. GO; GO:00005634; C:nucleus; IEA.
R. GO; GO:0005634; C:nucleus; IEA.
R. GO; GO:000155; F:DNA binding; IEA.
R. GO; GO:000135; P:ROBOLITY_12.
R. InterPro; IPR000135; Highmoblty_12.
R. InterPro; IPR000190; HMG 12_box.
R. PFEMI; PR00886; HIGHMOBLY12.
R. PRINTS; RR00886; HIGHMOBLY12.
R. RAMART; SM00198; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                         1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spalax Teucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                       International consortium for macaque cDNA sequencing, analysis; "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications."; submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
box 1 (HWGB1),...
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)...
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidee, Cercopithecinae; Macaca...
                                                                                                                                                                                                                        Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; Subanitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey CDNAs."; Submitted (NAR-2004) to the BMBL/GenBank/DDBJ databases. EMBL; AB166615; BAB00728.1; -; mRNA. SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1149; DB 2; Length 215; 100.0%; Pred. No. 6.9e-59; ive 0; Mismatches 0; Indels 0
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae; Spalacinae; Nannospalax.
NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High mobility group protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QX40_SPAEH PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              215; Conservative
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                    Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAEEKGKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
                                                                                                                                                                                                                                                                    MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                 EDMAKADKARYEREMKTY1PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPK1KGEHPGL
                                                                                                                                                                                                    Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bullerdies J., Nolte I.;
Bullerdies J., Nolte I.;
Bullerdies J., Nolte I.;
Wolecular characterization of the canine HWGB1.";
Cytogenet. Genome Res. 101:33-38 (2003).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA (By similarity).
-!- SUBCELULAR LOCATION: Notclear (By similarity).
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;
Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
                                                                                                                                    Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; DNA-Dinding; Nuclear protein; Repeat.
INIT_MET 0 0 P similarity.
                                                                                                                                                                                                    Indels
PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24895 WW; 599FB8A6FDF41F17 CRC64;
                                                                                                                                                                                                    ö
                                                                                                                                Score 1145; DB 2;
Pred. No. 1.2e-58;
1; Mismatches 0;
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EMBL; AY135521; AAN1319.1; -; Genomic_DNA.
HSSP; P07155; 1AAB.
RS, OGYKA4; 1-83, 92-170.
Ensembl; ENSCAFG0000006597; Canis familiaris.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG_12_box.
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PRINTS; PR00886; HIGHMOBLTY12.
                                                                                                                                    99.7%;
                                                                                                                             Query Match
Best Local Similarity 99.5
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                           1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                       DMAKADKARYEREMKTYI PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bbert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
"Cloning of human full open reading frames in Gateway(TM) system entry
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P09472; QGIBE1;
01-MAR-1989 (Rel. 10, Created)
01-ANG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
"The active gene that encodes human high mobility group 1 protein (HMG1) contains introns and maps to chromosome 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89160247; PubMed-2922262;
Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
"A human placental cDNA clone that encodes nonhistone chromosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhong X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1144; DB 1; Length 214; Pred. No. 1.3e-58;
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The German cDNA consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ji Q., Li R., Peng J., Jiang Y., Zho
to the EMBL/GenBank/DDBJ databases
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8 78 HMG box 1.
94 162 HMG box 2.
185 214 AB/Glu-rich (acidic).
214 AA, 24763 MW, B3C6A80FC7F0F433 CRC64;
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                                                                                                                                                                                                                                                                                                                                                    KKKKEEEEDEEDEEBEEBEEBEBBEEBDDDE 214
                                                                   99.6%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein HMG-1.";
Nucleic Acids Res. 17:1197-1214(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B1).
Name=HMGB1; Synonyms=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 35:367-371(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          He F.T., Yang Z.H., Ji
Submitted (SEP-2003) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                             Similarity
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                                                                                                           214;
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                DNA_BIND
COMPBIAS
SEQUENCE
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 DNA_BIND
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REAL TISSUE=Brain, Cervix, and Testis; Exclus MRNAI.

REAL TISSUE=Brain, Cervix, and Testis; MEDLINE=22388257; PubMed=12477925; DOI=10.1073/pnas.242603899; MEDLINE=22388257; PubMed=12477925; DOI=10.1073/pnas.242603899; REAL Strausberg R.L., Fetngold E.A., Grouse L.H., Derge J.G., Schuler G.D., Ratusner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altechul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K., RA Diatchenko L., Marushan R., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Stapleton M.J., McKernan K.J., Malek J.A., Galuarathe P.H., Richards S., McDwan P.J., McKernan K.J., Malek J.A., Glubs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., Rheby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shakesley R.W., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E., And Monse A.M., And Maria M.J., Warra M.A.; And Monse A.M., And Maria M.A.; And Monse A.M., And Maria M.A.; And Maria M., Marra M.A.; And Monse A.M., And Maria M.A.; And Monse M.A.; And Monse M.A.; And Monse M.A.; And Maria M.A.; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Mammary carcinoma;
MEDLINE=97295304; PubMed=9150946;
Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
Simpson R.J., Dorow D.S.;
Simpson R.J., Dorow D.S.;
"Two-dimensional electrophoretic analysis of human breast carcinoma
proctains: mapping of proteins that bind to the SH3 domain of mixed
lineage kinase MLK2.";
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Electrophoresis 18:588-598 (1997).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
                             Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM) system donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- INTERACTION:
P04637:TP53; NDExp=1; IntAct=EBI-389432, EBI-366083;
O15350:TP73; NDExp=1; IntAct=EBI-389432, EBI-389606;
-!- SUBCELLULAR LOCATION: Nuclear.
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                                                                                                      Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases

    -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family
    -!- SIMILARITY: Contains 2 HMG box DNA-binding domains

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EMBL; U51677; AAB08987.1; -; Genomic_DNA.
                                                                                                                                                      SCALE MRNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE OF 57-64 AND 112-126.
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CR749614; CAH18408.1; -; MRNA.
CR456863; CAG33144.1; -; MRNA.
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BT020159; AAV38961.1;
BC003378; AAH03378.1;
BC030981; AAH30981.1;
                                                                                                                                                         [LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
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SMR, P09429, 1-83, 92-170.
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H-InvDB; HIX0011209; -.
MIM; 163905; -.
                                                                                                                                                      SEQUENCE
                                                                                                                                                         NUCLEOTIDE
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Amphoterin.
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GO: GO: 0000793; C:condensed chromosome; IDA.

GO: GO: 0008301; F:DNA bending activity; TAS.

GO: 000062194; F:Lanscription factor binding; TAS.

GO: 000062194; F:Lanscription factor binding; TAS.

GO: 000062281; P:DNA recombination; TAS.

GO: 000062281; P:DNA recombination; TAS.

GO: 000062281; P:DNA recombination; TAS.

GO: 00006235; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 00006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 0006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 0006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 0006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 0006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

GO: GO: 0006325; P:Bestablishment and/or maintenance of chromat. .; TAS.

RIMTRY: SMO0398; HMG Dox. 1.

RNSTTE; PSS0118; HMG BOX 2; 2.

CHROMPOSOMAI PIND 94 162 HMG BOX 2.

FT DNA BIND 94 162 HMG BOX 2.

COMPENS 185 214 Asp/Glu-rich (acidic).

SEQUENCE 214 AA; 24763 MW; B33C6A80FC7F0F433 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWYTMSAKEKGKFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Spalacinae; Nannospalax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee K.-L.D., Lum H.-K., Nevo E.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR078819, AAC27652.1; -; Genomic_DNA.
HSSP, P07156; INHN.
SMR; O9QWY6; 2-84, 93-171.
GO; GO:0000785; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; P:DNA binding; IEA.
GO; GO:0006535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, I
01-MAR-2004 (TrEMBLrel. 26, I
High mobility group protein.
Name=HMG1;
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Best Local Similarity 100.
Matches 214; Conservative
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Ebkaryota; Metazos (Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
"Amphoterin is associated with the development of the kidney.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR275734; AAR27799.1; -; mRNA.
SEQUENCE 215 AA; 24894 MW; 8A868DBZ66D552B5 CRC64;
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99.4%; Score 1142; DB 2; Length 215;
Local Similarity 99.1%; Pred. No. 1.8e-58;
les 213; Conservative 2; Mismatches 0; Indels ()
                                                                                                                                                                                                                                         Query Match 99.4%; Score 1142; DB 2; Length 215; Best Local Similarity 99.5%; Pred. No. 1.8e-58; Matches 214; Conservative 0; Mismatches 1; Indels
                                                                                                                 PROSITE; PS00153; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24822 MW; D20D659274B575B4 CRC64;
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Last annotation update)
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InterPro; IPR000910; HMG 12_box.
Pfam: PF00505; HMG box: 2.
                            Pfam; PF00505; HMG box; Z. —
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
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ID Q548R9 RAT PRELIMINARY;
AC Q548R9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
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CSTRAINE-EVBN/N; TISSUE-Colon, and Mammary tumor. C3;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
ASTRAINE-EVBN/N; TISSUE-Colon, and Warmary tumor. C3;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
ASTRAUBENER R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
D. Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B.DOSA S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Bahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. Generation and initial analysis of more than 15,000 full-length human
                                                                                                 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
High mobility group box 1 (16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al3006401 product:high mobility group box 1, full insert sequence) (13 days embryo heart cDNA, RIKEN full-length enriched library, clone:B330050N16 product:high mobility group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2105566; PubMed=1127851; DOI=10.1038/35055500; MEDLINE=2105660; PubMed=1127851; DOI=10.1038/35055500; MEDLINE=2105660; PubMed=1127851; DOI=10.1038/35055500; MEDLINE=2105660; PubMed=1127851; DOI=10.1038/35055500; Medlingawa A., Shibata K., Yoshino M., Itohin Y., Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Oglobori T., Bono H., Kaeukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/67; TISSUE=Heart, and Thymus; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; Hidi-efficiency full-lengh cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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                               215 AA.
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                                                                               Created)
                                                                                                                                                                                                                                                            box 1, full insert sequence).
                                                                               10-MAY-2005 (TrEMBLrel. 30,
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                               OSBEVS MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                     Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE
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And Gustinacida S. Hills D. Knofmann W. Hume D. A. Kamiya W. L. Lea N. H. L. Dyons P. Marchinoni L. Mashima J. Mazzaralii J. Monbactor P. Marchinoni L. Mashima J. Mazzaralii J. Monbactor P. Marchinoni L. Mashima J. Salaci E. Safancor N. T. Shakara H. Satok H. Schochaberl C. Saya T. Shibata Y. Scorch K. F. Sanki H. Satok H. Schochaberl C. Saya T. Shibata Y. Scorch K. F. Shibata H. Satok H. Sanki H
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    R. STRAIN-GSTBL/GGJ; TISSUB-Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Hayashida K., Hayatu M., Hiramoto K., Hiraoka T., Hiraozane T.,
Hayashida K., Hayatu M., Hiramoto K., Hiraoka T., Kaluwa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanukawa T.,
RA Katch H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki R., Oanno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki R., Oanno H., Kouda M., Koya S.,
RA Kurihara C., Sattoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Satto R., Sattoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Sasaki D., Shibata K., Yakaunishi A., Muramatsu M., Hayashizaki Y.;
RA Sasaki D., Shibata K., Sanunishi A., Muramatsu M., Hayashizaki Y.;
REMEL, BC091741, AAH9174111; J. MRNA.
BEMEL, RC0910301, AAH90174111; J. MRNA.
BEMEL, AK037928; BAC299021; J. MRNA.
BEMEL, AK037928; BAC299021; J. MRNA.
BREMEL, AK037928; BAC299021; J. MRNA.
BREMEL, AK037928; BAC299021; J. MRNA.
BREMEL, MC037039; FINITI-C-oxide biosynthesis; IDA.
GO; GO:0005613; F:protein binding; IPI.
BR GO; GO:0005613; F:protein binding; IPI.
BR GO; GO:0006513; F:protein binding; IPI.
BR GO; GO:0006503; HMG I2_box.
BR RINTS; PR00886; HIGHWBLY12.
BR SRRT; SR00886; HIGHWBLY212.
BR SRRT; SR00886; HIGHWBLY212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGDVAKKLGEMWNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
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                                           Σ.
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Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
B1).
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PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24894 MW; 8A868DE266D552B5 CRC64;
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Matches 213; Conservative
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                                                                                                                NUCLEOTIDE SEQUENCE.
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ID HMG1_BOV

AC P10103;

DT 01-MAR-1:

DT 13-SEP-2:

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE-811389848; Pubmed=7202717; DOI=10.1016/0014-5793(80)80453-4;
Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
"The primary structures of non-histone chromosomal proteins HMG 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6; Christen T., Bischoff M., Hobi R., Kuenzle C.C.; Fill Mediated T., Bischoff M., Hobi R., Kuenzle C.C.; Fill Mediated Dologous proteins 1 and 2 bind preferentially to brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not to other types of Z-DNA."; PEBS Lett. 267:139-141[1990).

-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
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Pentecost B., Dixon G.H.;
"Isolation and partial sequence of bovine cDNA clones for the high-mobility-group protein (HMG-1).";
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Holstein; TISSUB=Fetal thymus;
BRDILNE=8957489; PubMed=3194213;
Kaplan D.J., Duncan C.H.,
"Full length cDNA sequence for bovine high mobility group 1 (HMG1)
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RGO; GO:000793; C:condensed chromosome; ISS.

RGO; GO:0007931; F:DNA bending activity; ISS.

RGO; GO:0006281; F:protein binding; ISS.

RGO; GO:0006288; P:base-excision repair, DNA ligation; ISS.

RGO; GO:0006281; P:DNA repair, ISS.

RGO; GO:0006281; P:DNA repair, ISS.

RGO; GO:0006282; P:DNA repair, ISS.

RGO; GO:0006282; P:DNA repair, ISS.

RGO; GO:0006282; P:DNA unwinding; ISS.

RGO; GO:0006282; P:DNA unwinding; ISS.

RGO; GO:0006282; P:ROPALISHMENT and/or maintenance of chromat. ...

RGO; GO:0006315; P:ROPALISHMENT and/or maintenance of chromat. ...

RGO; GO:001055; P:ROPALISHMENT AND/OR MAINTENANCE CHROMAT. ...

REPROS | PROMOSOS | P:ROPALISHMENT | P:ROPALISH | P:ROP
                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Cetartiodactyla; Ruminantia;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos
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SWART, SM00398, HMG, 2.
PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; Direct protein sequencing; DNA-binding;
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-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 16:10375-10375(1988).
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EMBL; M26110; AAA30567.1; -; mRNA.
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INIT MET 0 0
DNA_BIND 8 78
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Bos taurus (Bovine)
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Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
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98.6%; Pred. No. 3e-58;
ive 3; Mismatches
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088612;
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Best Local Similarity 98.6
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                            Name=HMG1;
                                                                                                        181
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                             Gaps
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SMR; O88611; 2-84, 93-171.
GO; GO:000785; C:chromatin; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:Pregulation of transcription, DNA-dependent; IEA.
InterPro; IPR000910; HMG 12 box.
InterPro; IPR000910; HMG 12 box.
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                                                                                                                                                                99.2%; Score 1140; DB 1; Length 214; 99.5%; Pred. No. 2.3e-58; ive 1; Mismatches 0; Indels
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                   Asp/Glu-rich (acidic).

C -> S (in Ref. 3).

C -> A (in Ref. 3).

EHPGL -> PGGGV (in Ref. 2).

E -> D (in Ref. 3).
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO78B17; AAC27650.2; -; Genomic_DNA.
HSSP; P07156; 1NHN.
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PRINTS; PR00886; HTGHMOBLTY12.
SMART; SM00398; HMG; 2. 2.
PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24905 MW; 64816B6FCF6033EA CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
High mobility group protein.
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Best Local Similarity 99.5
Watches 213; Conservative
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088611;
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94 1
185 2
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105 1
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214 AA;
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DNA BIND
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SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                           61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Spalacinae, Nannospalax.
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P63158; P07155; P27109; P27428;
01-APR-1988 (Rel. 07, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation property protein B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee K.-L.D., Lum H.-K., Nevo E.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078918; AAC27651.1; -; Genomic_DNA.
HSSP; P07156; JNHN.
SKR; O88612; 2-84; 93-171.
GO; GO:0000785; C:chromatin; IEA.
GO; GO:0005634; C:uncleus; IEA.
GO; GO:000557; F:DNA binding; IEA.
GO; GO:0006355; P:requlation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmobly 12.
InterPro; IPR000135; Highmobly 12.
InterPro; IPR000135; HMG_12_box.
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Last annotation update)
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U00431; AAA20508.1; -; mRNA
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MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHORLO, L., Marusina K.M., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Radan A., Woung A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Mederatise of Maryanski M.I., Skalaka U., Smailus D.E.,

"Manan Maryan M.A., Maray M.A., Marra M.A.;

"Mederatise of Maryanski M.I., Skalaka U., Smailus D.E.,

"Manan M.A., Manalysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
"Molecular cloning, expression analysis, and chromosomal localization of mouse Hagl-containing sequences.";
Manm. Genome 5:91-99(1994).
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBSECTIONAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material. SIMILARITY: Belongs to the HWG1/FWG2 protein family. SIMILARITY: Contains 2 HMG box DNA-binding domains.
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MEDLINE=95050689; PubMed=7961836;
MEDLINE=95050689; PubMed=7961836;
MEDLINE=95050689; PubMed=7961836;
"The mouse gene coding for high mobility group 1 protein (HMG1).";
J. Biol. Chem. 269:28803-28808(1994).
                                                                                                                                                                                                                                                                                                                                      MEDLINE=92335012; PubMed=1630928;
Yotov W.V., St Arnaud R.;
"Nuclectide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group protein-1 (HMG1).";
Nucleic Acids Res. 20:3516-3516(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ghosh B.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
   Name=Hmgbl; Synonyms=Hmg-1, Hmgl;
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                                           Mus musculus (Mouse).
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EMBL; Z11997; CAA78042.1; -; mRNA.

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P63159; P07155; P27109; P27428;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HWG-1) (High mobility group protein 1 (Amphoterin) (Heparin-binding protein p30).
Name-Hmgbl; Synonyms-Hmg-1, Hmgl;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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                               SWART: pruchase, m.v. PROSITE; PS00155; HMG BOX 1; 1. PROSITE; PS00118; HMG BOX 2; 2. PROSITE; PS50118; HMG BOX 2; 2. Chromosomal protein; DNA-Binding; Heparin-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurogna
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1137; DB 1; Length 214;
Pred. No. 3.4e-58;
2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24763 MW; B3C6A91FD6F1B133 CRC64;
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E -> V (in Ref. 4).
D -> E (in Ref. 3).
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X80457; CAA56631.1; -; Genomic_DNA.
L38477; AAA57042.1; -; mRNA.
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HMG box 1.
HMG box 2.
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MEDLINE=88067717; PubMed=3684582;
                                                                                                                                                                                                                                                                                                        InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box: 2
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SMR; P63159; 1-83, 92-170.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                 "The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal sequence and production of antipeptide antibodies that detect p30 at the surface of neuroblastoma cells and of brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spectroscopy.";
Biochemistry 34:16596-16607(1995).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
-!- FUNCTION: Binds preferentially single-stranded DNA are a role in
double stranded DNA. Heparin-binding protein that has a role in
the extension of neurite-type cytoplasmic processes in developing
cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley;
MEDLINE-96118376; PubMed-8527432;
Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
Thomas J.O., Laue B.D.;
"Structure of the A-domain of HMG1 and its interaction with DNA as
studied by heteronuclear three- and four-dimensional NMR
                                                                                                                                             MEDLINE=91358468; PubMed=1885601;
Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala "30-kDa heparin-binding protein of brain (amphoterin) involved in neutric outgrowth. Amino acid sequence and localization in the filopodia of the advancing plasma membrane.";
J. Biol. Chem. 266:16722-16729(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 87-164.
MEDLINE=93233672; PubMed=8467791;
MEDLINE=9323672; FubMed=8467791;
Thomas J.O.;
Thomas J.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the HMG box motif in the B-domain of HMG1."; EMBO J. 12:1311-1319(1993).
                                                                                   Bianchi M.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUB-Kidney, Prostate, and Testis;
NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE
Paonessa G., Frank R., Cortese R.; "Nucleotide sequence of rat liver HMG1 cDNA."; Nucleic Acids Res. 15:9077-9077(1987).
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EMBL; Y00463; CAA68526.1; -; mRNA.
EMBL; BC061779; AAH61179.1; -; mRNA.
EMBL; BC081839; AAH81839.1; -; mRNA.
EMBL; BC088402; AAH81830.1; -; mRNA.
PIR; A41175; NSRTH1.
PDB; LAAB; NMR; @=183.
PDB; LCKT; X-ray; A=7-77.
PDB; 1HME; NMR; @=88-164.
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                                                                  SEQUENCE REVISION
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
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                                                                                                                         PROSITE; PS00153; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
3D-structure; Chromosomal protein; Direct protein sequencing; DNA-binding; Heparin-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%; Score 1137; DB 1; Length 214; 99.1%; Pred. No. 3.4e-58; ive 2; Mismatches 0; Indels (
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Last annotation update)
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HMG box 2.
Asp/Glu-rich (acidic)
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                           InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG 12_box.
Pfam; PP00505; HMG box; 7.
SPRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
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Q6P202;
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hes 212; Conservative
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             RGD; 2802; Hmgb.
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,
A Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worlby K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W.,
A Willing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenrach A., Schein J.E., Jones S.J.M., Marra M.A.;
Tand mouse CDNA sequences.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC064730, AAH64790.1; -; mRNA.

R HSSP; P07155; 1AAB.

R MG1; MG1:96113; Hmgbl.

R G0; G0:0005615; C:extracellular space; IDA.

G0; G0:0005615; C:extracellular space; IDA.

G0; G0:0005615; F:protein binding; IPI.

R G0; G0:0006810; P:nitric-oxide synthase regulator activity; IDA.

G0; G0:0006810; P:nitric oxide biosynthesis; IDA.

R G0; G0:0006810; P:transport; IDA.

R G0; G0:0006810; P:transport; IDA.

R HITCEPTO; IPR00019; Highmoblty_12.

R InterPro; IPR00019; Highmoblty_12.

R PFRM; PFROSOS, MG POX. 2.
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PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Embryo;
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01-AUG-1990 (Rel. 15, Last seqn
13-SEP-2005 (Rel. 48, Last ann
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SMART; SM00398; HMG; 2.
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01-AUG-1990 (Rel. 15, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) High mobility group protein 1 (HMG-1) (High mobility group protein

Name=HMGB1; Synonyms=HMG1; Sus scrofa (Pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 27:6159-6163(1988).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
-!- SUBCELLULAR LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                       Tsuda K.-I., Kikuchi M., Mori K., Waga S., Yoshida M.; "Primary structure of non-histone protein HMG1 revealed nucleotide sequence.";
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B29C8A32D8D2C933 CRC64;
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PIR; A28897; A28897.
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6, 2006, 10:25:39 ; Search time 61.5296 Seconds (without alignments) 288.890 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	US-09-538-092-883	US-09-214-881A-1	US-09-214-881A-3	US-09-214-881A-4	US-09-214-881A-5	US-09-949-016-10813	US-09-949-016-10728	US-09-538-092-1018	US-09-214-881A-2	US-09-214-881A-6	US-09-214-881A-8	US-09-214-881A-9	US-09-214-881A-11	US-09-914-259-38	US-09-214-881A-10	US-09-702-705-789	US-09-736-457-789	US-09-614-124B-789	US-09-671-325-789	US-09-589-184-789	US-09-658-824-789	US-10-017-754-789	US-09-651-563-789	US-09-519-642-789	US-09-949-016-10496	US-09-702-705-1667	US-09-736-457-1667
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US-09-614-124B-1667 US-09-671-325-1667	US-09-658-824-1667	US-10-017-754-1667	US-10-017-754-1913	US-09-651-563-1667	US-09-702-705-324	US-09-736-457-324	US-09-614-124B-324	US-09-671-325-324	US-09-589-184-324	US-09-658-824-324	US-10-017-754-324	US-09-651-563-324	US-09-519-642-324	US-09-214-881A-7	US-09-513-999C-4824	US-09-513-999C-4825
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ALIGNMENTS

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DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120
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                                                            APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PLING DATE: 1999-04-01
PRIOR PLING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPat/SeqFormatter Version 0.9
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OTHER INFORMATION: Polypeptide Accession Number P09429
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100.0%; Pred. No. 2.3e-100;
tive 0; Mismatches 0;
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Sequence 883, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 214; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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RESULT 2 US-09-214-881A-1 121

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61 DWAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120
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  0; Gaps
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APPLICANT: Caski, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Taraka, Masao
APPLICANT: Taraka, Masao
APPLICANT: Taraka, Masao
APPLICANT: Taraka, Mitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
APPLICANT: Shirakawa, 1104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTING DATE: 1999-06-07
MUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTING DATE: 1999-06-07
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Pred. No. 1.6e-99;
1; Mismatches 1;
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Best Local Similarity 99.1%;
Matches 212; Conservative
  213; Conservative
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US-09-214-881A-5
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                                                                          APPLICANT: OZAKI, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TILLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06033.0.04
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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GENERAL INFORMATION:
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funio
TILE REFERENCE: O68383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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Sequence 1, Application US/09214881A
Patent No. 6822078
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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; ORGANISM: Bos taurus
US-09-214-881A-3
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Best Local Similarity
                                Patent No. 6822078
GENERAL INFORMATION:
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LENGTH: 214
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181 SKKKKEEEEDEEDEEDEEDEEDEEDE 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-09-949-016-10728
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; ORGANISM: Human
US-09-949-016-10728
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LENGTH: 320
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; Patent No. 6812339
; GENERAL INCORMATION:
; PAPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WINDER: US/09/949,016
; CURRENT APPLICATION NUMBER: 06/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10813
; LENGTH: LANDER OF THE CONTRACT OF THE
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APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
FURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 214
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Best Local Similarity 94.8
Matches 201; Conservative
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Best Local Similarity
Matches 210; Conserv
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ORGANISM: Human
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Sequence 10728, Application US/09949016

| Sequence 10728, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR PILING DATE: 2000-10-20
| PRIOR PILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFFWARE: PERSESEQ FOR Windows Version 4.0
123 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 182
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APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT FILING DATE: 2000-03-29
RRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
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DB 2;
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Best Local Similarity 81.4%; Pred. No. 2.3e-79;
Matches 171; Conservative 18; Mismatches 20
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                                                                             182 KKKKEEEEDEEDEEDEEEEDEEDEE
                                                                                                                                                                                  Sequence 6, Application US/09214881A
Patent No. 6822078
GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
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ORGANISM: Sus scrofa
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Hiroko
APPLICANT: Usugaj, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIGGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOSTWARE: Patentin Ver. 2.1
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                                                                                                                                                                    LOCATION: (0).7.(0)
CTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
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                 NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1018
LENGTH: 208
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   PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                   NAME/KEY: misc feature
                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 208
TYPE: PRT
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61 DMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLS 120
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APPLICANT: Ozadi, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usadi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
: TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 209;
APPLICANT: Shirakawa, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shakawa, Hitoshi
APPLICANT: Obakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
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61 DLAKSDKACYYREMKNYVSPKGDKKKKDPNAPKRPPSAFCLFCSENRPKIKIEYPGLS 120
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                                                                                                                                                       APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Geugi, Hiroko
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Massao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Rumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%; Score 827; DB 2; Length 20
74.0%; Pred. No. 2e-70;
ive 23; Mismatches 31; Indels
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; Patent No. 649536
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; TURRENT APPLICANION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENOTH 879
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181 KKKNDSEDEEEEEEEEEEDEEGEEEDEE 208
181 KKKABPEEEEEEEDEEEEEEEDEE 206
                                                                                               Sequence 11, Application US/09214881A Patent No. 6822078
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US-09-914-259-38
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Best Local Similarity
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                                                                             US-09-214-881A-11
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                                                                                                                                                                  DB 2; Length 209;
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VENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
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                                                                                                                                                                  79.7%; Score 915.5; DB 2; Length : 80.5%; Pred. No. 8.6e-79; Live 19; Mismatches 21; Indels
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APPLICANT: Osakada, Fumio
TITLE OP INVENTION: DIAGNOSTIC DRUGS FOR I
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
NUMBER OF SEQ ID NOS: 13
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Sobajima, Junko
Ueugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakoo, Kazuwa
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Shirakawa, Hitoshi
                       Patentin Ver. 2.1
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Matches 165; Conservative
                                                                                                                                                                Query Match
Best Local Similarity 80.5
Matches 169; Conservative
                                                                                  TYPE: PRT ORGANISM: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Gallus gallus
NUMBER OF SEQ ID NOS:
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SOFTWARE: Pate
SEQ ID NO 9
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US-09-214-881A-9
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                                         SEQ ID NO 8
LENGTH: 209
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                               120 GDVAKKLGEMWNNLSDGEKQPYNNKAAKLKEKYEKDVADYKSKGKFDGAKGA---ATKAA 176
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20 VQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYI 79
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usazaki, Hiroko
APPLICANT: Usazaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Gaskada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                   ; Sequence 10, Application US/09214881A; Patent No. 6822078; GENERAL INFORMATION:
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; Sequence 1, Application US/10147447; Publication No. US20030060410A1; GENERAL INFORMATION:
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Sequence 22, P
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; Sequence 1446, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
    APPLICANT: Brgelhard, Eric K.
    TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OCANCER
    FILE REFERENCE: 52945200012.
    CURRENT APPLICATION NUMBER: US 09/747,377
    PRIOR APPLICATION NUMBER: US 09/747,377
    PRIOR APPLICATION NUMBER: US 09/747,377
    PRIOR FILING DATE: 2000-12-22
    NUMBER OF SEQ ID NOS: 2059
    NUMBER: FASELSEQ for Windows Version 4.0
    SEQ ID NO 1446
    LEAGTH: 215
    LEAGTH: 215

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US-10-726-195-5
US-10-730-072-18
US-10-300-072-24
US-10-456-949-18
US-10-456-947-6
US-10-718-495-18
US-10-718-495-18
US-10-718-495-18
US-10-718-495-18
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US-10-718-495-18
US-10-718-495-18
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US-10-456-947-12
US-10-718-495-25
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Best Local Similarity 100.
Matches 215; Conservative
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Sequence 1, Application US/1030072

Publication No. US20030144201A1

GENERAL INFORMATION:

APPLICANT: Revin J. Tracey

APPLICANT: Huan Yang

APPLICANT: Mitchell P. Fink

ITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY

TITLE OF INVENTION: AGENTS

FILE REFERENCE: 3268.1001-005

CURRENT APPLICATION NUMBER: US/10/300,072

CURRENT FILING DATE: 2002-11.20

FRIOR FILING DATE: 2002-11.20

FRIOR FILING DATE: 2002-05-15

FRIOR FILING DATE: 2002-05-15

FRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FREAERC for Windows Version 4.0

SEQ ID NOS: 58
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100.0%; Pred. No. 3.6e-70;
iive 0; Mismatches 0;
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                   APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Warren Jr., Howland Shaw
TITLE OF INVENTION: Use of HMG Fragments as
TITLE OF INVENTION: Anti-Inflammatory Agents
FILE REPRENCE: 3268-1001-001
CURRENT APPLICATION NUMBER: US/10/147,447
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
APPLICANT: Tracey, Kevin J. APPLICANT: Yang, Huan
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Best Local Similarity 100.
Matches 215; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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Matches 215; Conserv
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                                    61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
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Publication No. US20040053841A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
TITLE OF INVENTION: HMIBITORS OF THE INTERACTION BETWEEN
TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
TITLE OF INVENTION: AMTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3268.1001-007
CURRENT APPLICATION NUMBER: US/10/456,947
CURRENT FILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 10/147,447
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100.0%; Pred. No. 3.6e-70;
iive 0; Mismatches 0;
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GENERAL INVENTATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Huan Yang

TITLE OF INVENTION: USE OF HMG FRACHENTS AS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

FILE REFERENCE: 3268.1001-006

CURRENT APPLICATION NUMBER: US/10/456,949

CURRENT FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR PILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 215
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Best Local Similarity 100.
Matches 215; Conservative
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 215; Conservative 0
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                                                                                                                                                                                                                                                                                               LENGTH: 215
TYPE: PRT
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; Publication No. US20040141948A1
; GENERAL INFORMATION:
; TTILE OF INVENTION: USE OF HAGB FRAGMENTS AS
; TTILE OF INVENTION: ATTILINGAMMATORY AGENTS
; TTILE OF INVENTION: ATTILINGAMMATORY AGENTS
; TITLE OF INVENTION: ATTILINGAMMATORY AGENTS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT APPLICATION NUMBER: 60/427,841
PRIOR FILING DATE: 2003-11-20
; ROFTWARE FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 1
LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-495-1
                                                                                                                                                                                                                                         0; Mismatches
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                         Matches 215; Conservative
                                                                                                             LENGTH: 215
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                  US-10-456-947-1
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US-10-718-495-1
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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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; Sequence 63, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION:
    FILE REFERENCE: 28967/33359A
; CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/478,390
PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR PILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SEQ ID NO 63
; LENGTH: 215

**WAPPL TO 1158
**COFTWARE: PATENTIN VERSION 3.2
; SEQ ID NO 63
**COFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1149; DB 4;
100.0%; Pred. No. 3.6e-70;
tive 0; Mismatches 0;
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; Pred. No. 3.6e-70;
0; Mismatches 0;
Sequence 1, Application US/10717984

Publication No. US20040156851A1

GENERAL INPORMATION:

APPLICANT: Newman, Walter

TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES

FILE REFERENCE: 3258.1008-001

CURRENT FILING DATE: 2003-11-20

PRIOR PILITGATION NUMBER: 60/427,846

PRIOR PLICATION NUMBER: 60/427,846

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SOFTWARE PEACES FACTOR WINDOWS VERSION 4.0
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Length 215;

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100.0%;
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Best Local Similarity 100.0
Matches 215, Conservative
  LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-938-992-38
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                                                                                      SIGDVAKKLGEMMINITAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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PUblication No. US20050043235A1

GENERAL INFORMATION:

APPLICANT Alitalo et al.

TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
FILE REPERENCE: 29967/3917A

CURRENT APPLICATION NUMBER: US/10/868,549

CURRENT FILING DATE: 2004-06-14

PRIOR FILING DATE: 2003-06-12

PRIOR FLING DATE: 2003-06-12
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APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
APPLICANT: Obar, Robert
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REFERENCE: 3258.1033-001
CURRENT PELLING DATE: 105/10/938,992
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: 60/502,568
PRIOR FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FASELSEQ for Windows Version 4.0
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100.0%; Pred. No. 3.6e-70;
iive 0; Mismatches 0;
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US-10-938-992-74
US-10-938-992-74
; Sequence 74, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
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Best Local Similarity 100.0
Matches 215; Conservative
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: LENGTH: 215

: TYPE: PRT

: ORGANISM: Homo sapiens

US-10-868-549-22
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US-10-868-549-22
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Pred. No. 6.7e-70;
1; Mismatches 0; Indels
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; Score 1149; DB 5;
; Pred. No. 3.6e-70;
0; Mismatches 0;
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US-09-214-881A-1
; Sequence 1, Application US/09214881A
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Best Local Similarity 99.5
Matches 214; Conservative
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DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAPFLFCSEYRPKIKGEHPGLS 120
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                                                                                                                                                                          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                   2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Newman, Walter
APPLICANT: Qin, Shixin
APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REPERENCE: 3258-1033-001
FILE REPERENCE: 2004-09-10
FILE REPERENCE: 2004-09-10
FRICA PAPLICATION NUMBER: 60/502,568
FRICA FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SEQ ID NOS: 76
SEQ ID NO 40
LENGTH: 221
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                                                           Best Local Similarity 100.0%; Pred. No. 7.8e-70; Matches 214; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10938992; Publication No. US20050152903A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: rec-HMGB1-His6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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Jeal Carri, Shoichi
Jeal Carri, Shoichi
Sobalima, Junko
APPLICANT: Usugi, Hiroko
APPLICANT: Usugi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Punio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06833.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver 7
SEQ ID NO: LENGTH:
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Useudi, Hiroko
APPLICANT: Useudi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Ostada, Funio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: 06833.0104
CURRENT PRIJING DATE: 2003-12-02
CURRENT PRIJING DATE: 1999-06-07
PRIOR APPLICATION NUMBER: US/09/214,881A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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100.0%; Pred. No. 7.8e-70;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 214; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-1
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LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
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## APPLICANT: Warren Jr., Howland Shaw
## APPLICANT: Warren Jr., Howland Shaw
## TITLE OF INVENTION: Use of HAG Fragments as
## TITLE OF INVENTION: Anti-Inflammatory Agents
## TITLE OF INVENTION: Anti-Inflammatory Agents
## FILE REPRENCE: 3260.001-001
## PRIOR APPLICATION NUMBER: 0202-00-16
## PRIOR APPLICATION NUMBER: 02005, 10:32:46
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## PRIOR APPLICATION NUMBER: 0200-00-16
## PRIOR APPLICATION NUMBER: 02005, 10:32:46
## PRIOR APPLICATION NUMBER: 0200-00-16
## PRIOR APPLI
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RESULT 2
US-11-186-422-11
Sequence 11, Application US/11186422
; Publication No. US20060057679A1
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1234, Ap
1234, Ap
11234, Ap
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113, Appl
1153, Ap
1101, Ap
                                                                                                                                          April 6, 2006, 10:28:08 ; Search time 26.875 Seconds (without alignments) 249.536 Million cell updates/sec
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Sequence 6
Sequence 1
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8: /SIDS5/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-172-740-1566
US-11-087-099-9185
US-11-087-099-11126
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US-11-186-422-11
US-11-169-041-192
US-10-821-234-1234
US-10-11-86-422-14
US-10-11-86-422-13
US-11-186-422-13
US-11-186-422-13
US-11-087-099-8879
US-11-087-099-3510
US-11-087-099-3510
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US-11-172-740-1572
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Maximum DB seq length: 2000000000
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	Sequence 32735, A Sequence 32734, A	Sequence 32733, A Sequence 13611, A	Sequence 26884, A Sequence 26883, A		Sequence 3510, Ap	Sequence 21031, A	Sequence 21033, A	Sequence 21032, A	Seguence 3511, Ap	Sequence 9681, Ap	Sequence 9680, Ap	Sequence 869, App	Sequence 9518, Ap	Seguence 8838, Ap	Sequence 308, App
US-11-172-740-1565 US-11-087-099-5374	US-11-096-568A-32735 US-11-096-568A-32734	US-11-096-568A-32733 US-11-096-568A-13611	US-11-096-568A-26884 US-11-096-568A-26883	US-11-172-740-1564	US-11-096-568A-3510	US-11-096-568A-21031	US-11-096-568A-21033	US-11-096-568A-21032	US-11-096-568A-3511	US-11-096-568A-9681	US-11-096-568A-9680	US-11-087-099-869	US-11-087-099-9518	US-11-087-099-8838	US-11-124-368A-308
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26	28 29	30 31	32	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT PAPLICATION NUMBER: US/10/821,234
CURRENT PAPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PLING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1443
LENGTH: 215
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; Sequence 1443, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-821-234-1443
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1234
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Publication No. US20050255114A1
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; ORGANISM: Homo sapiens
US-11-169-041-192
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US-10-821-234-1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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      GENERAL INFOGRALIAUS:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Theresa
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Qin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT FILING DATE: 2005-07-20
PRIOR FILING DATE: 2005-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 215
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US-11-13

Sequence 12, Application US/11186422

Publication No. US20060057679A1

GENERAL INFORMATION:

APPLICANT: Critical Theresa

APPLICANT: Ordefe, Theresa

APPLICANT: Qin, Shixin

TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES

FILE REFRENCE: 3258-1021-003

CURRENT APPLICATION NUMBER: US/11/186,422

CURRENT APPLICATION NUMBER: US/11/186,422

CURRENT APPLICATION NUMBER: 60/589,678

PRIOR FILING DATE: 2005-07-20
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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LENGTH: 215
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Squence 192, Application US/11169041

Squence 192, Application US/11169041

Squence 192, Application US. US20060019284A1

GENERAL INFORMATION:

JENUTIANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE

TITLE OF INVENTION: CELLS

TITLE OF STORE TOOL NP

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT APPLICATION NUMBER: 60/584,405

PRIOR PILING DATE: 2004-06-30

NUMBER OF SEQ ID NOS: 527

SQOFTWARE: Patentin version 3.2

LENGTH: 879
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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                 121 SIGDVAKKLGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                             121 SIGDVAKKIGEMMNNTAADDKQPYEKKAAKIKEKYEKDJAAYRAKGKPDAAKKGVVKAEK
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang X. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYI
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Gaps 82 54

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1 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET
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Publication No. US20060041961A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT RILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.0%; Score 287; DB 6; L
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 54; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 54; Conservative 0; Mismatches 0;
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Sequence 13, Application US/11186422;
Publication No. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Luciano, Peter
APPLICANT: Qin, Shixin
TILE REFERENCE: 3258.1021-003
FILE REFERENCE: 3258.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT APPLICATION NUMBER: 05/589,678
PRIOR FILING DATE: 2005-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 54
PRIOR APPLICATION NUMBER: US/10/300,068
PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20
PRIOR PLING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 10/210,747
PRIOR PRILING DATE: 2000-02-14
PRIOR PRILING DATE: 2000-02-14
PRIOR PRILING DATE: 1990-02-14
PRIOR PLING DATE: 1999-02-11
PRIOR PLING DATE: 1999-02-11
SAPPLICATION NUMBER: US 09/248,574
PRIOR PLING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PRESER FOR WINDOWS VERSION 4.0
SEQ ID NO 6
LENGTH: 54
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US-10-719-150-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKIGEMMNNTAADDKQPYEKKAAKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                   1 SSYAFFVQTCREEHKKKHPDSSVNPAEFSKKCSERWKTMSAKEKSKFEDMAKSDKARYDR
                                                                                                                                                                                                                                                                                                                                                                   14 SSYAFFVQTCREEHKKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYER
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                              Query Match 59.3%; Score 681; DB 6; Length 169; Best Local Similarity 75.1%; Pred. No. 3.2e-43; Matches 127; Conservative 13; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 32.2%; Score 370; DB 7; Length 69; I Similarity 100.0%; Pred. No. 6.4e-21; 69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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; Publication No. US20040120953A1
; GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
; APPLICANT: Haichao Wang
; TITLE OF INVENTION: ANTACONISTS OF HMGI FOR TREATING
; TITLE OF INVENTION: INFLAMMATORY CONDITIONS
; FILE REFERENCE: 3268,1000-011
; CURRENT APPLICATION NUMBER: US/10/719,150
                                                                                                                             NAME/KEY: misc_feature; LOCATION: (1)...(169); OTHER INFORMATION: Xaa = any amino acid or nothing US-10-821-234-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/11186422
Publication No US20060057679A1
GENERAL INPORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Thereaa
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT PILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR FILING DATE: 2004-07-20
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 69
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                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKYEKDIAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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US-10-719-150-6
                                LENGTH: 169
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                                                                                                             FEATURE:
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OTHER INFORMATION: Utility: Useful for making plants with increased biomass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 KADKARYEREMKTYIPPKG-----ETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 -GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- 106
                                                                                                                                                                                                                                                                                                                                                                  2 KGGKSKAKSDNKLAVKKRGCETKKSKKSVKDPNKPKRRPPSAFFVFMEDFRKTYKEKHPNN
                                                                                                                                                                                                                                                                                                                             120 LSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAE
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UG-11-087-099-3510
; Sequence 3510, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REPRENCE: 38-21 (53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3510
                                                                                                                                                            53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(5/3450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 141
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23.8%; Score 273; DB 7;
Best Local Similarity 37.3%; Pred. No. 1.7e-13;
Matches 56; Conservative 31; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.3%; Score 268; DB 7; Best Local Similarity 39.2%; Pred. No. 3.8e-13; Matches 62; Conservative 23; Mismatches 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 KSKKKKEEEEDEEDEEDEEEEDEEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3073, Application US/11087099
Publication No. US20060041961A1
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US-11-087-099-3073
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                                                     US-11-172-740-1569
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  LOCATION:
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APPLICANT: MASCALLA, Peter
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyachedlav
TITLE OF INVENTION: NUCLEOFILE
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE REFERENCE: 2750-1602PUS2
CURRENT APPLICATION NUMBER: 08/11/172,740
CURRENT FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
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OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowe:
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                                                                                                                                                                                                 279 KKTKKEKDPLKPKHPVSAFFLFMNERRADLVAEKK--NVLEVGKITGEEWKNMTEKEKAP 336
                                                                                                                                                                                                                                                                                                                             219 KKPYÉBKYQAEKEAYLKIVGAEKRENBAMKLLÉEEQKQRTAMELLEQYMQFKEETENDKK 278
                                                                                                                                                                                                                                                                                                                                                                                ---KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 YEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSK------KKKEEEEDEED 193
                                                                                                                                                            1 MGKGDPKK--PRGKMSS--YAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKE
                                                                                                      51;
                                                        Length 502;
                                                   24.2%; Score 278.5; DB 7; Length 31.8%; Pred. No. 2.5e-13; ive 39; Mismatches 86; Indels
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OTHER INFORMATION: Public GI no. 1052956
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                                                                                                                                                                                                                                                                          KGKFEDMAKADKARY------
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                                                                                                           Conservative
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NAME/KEY: misc_feature
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ORGANISM: Glycine max
                                                   Query Match
Best Local Similarity
Matches 82; Conserv
US-11-087-099-8879
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US-11-172-740-1569
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62 KSVAAVGKAGGDAWKKLSEAEKAPYQAKAEKRKAEYQKNMDAYNRKQAGDA-----BED 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 IKGEHP-GLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAA 171
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                             KGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 AKSKG----AAKADTKLAVKSKGAEKPAAKGKKGKAGKDPNKPKRAPSAFFVFMGEFREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 160;
                                                          US-11-087-099-4976; Application US/11087099; Sequence 4976, Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION: APPLICANT: Abad, Mark S. et al.; TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(55450) B EP; CURRENT APPLICATION UNMERR: US/11/087,099; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 4976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 KKGVVKAEKSKKKKEEEEDEEDEEDEEEEEBDEBDEEBDDDE 215
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                                                                                                                                                             173 KGVVKAEKSKKKKEEEDBEDEEDEEDEEDEBDEDEEEDDDD 214
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERROR: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.3%; Score 267.5; DB 7
Best Local Similarity 39.6%; Pred. No. 4.8e-13;
Matches 65; Conservative 24; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Hordeum vulgare subsp. vulgare US-11-087-099-1105
                                                                                                                                                                                                                                                                                                     Sequence 1105, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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US-11-087-099-4976
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Best Local Similarity
Matches 56; Conserv
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                             114
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1571, Application US/11172740

| Sequence 1571, Application WG20060057724A1
| Sequence 1571, Application WG20060057724A1
| GENERAL INFORMATION:
| APPLICANT: MASCIA, Peter
| APPLICANT: MASCIA, Peter
| APPLICANT: MASCIA, Vyacheelav
| TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PHENOTYPES
| TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PHENOTYPES
| TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
| TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
| TITLE OF INVENTION: NUMBER: 05/583,621
| PRIOR PELLING DATE: 2004-06-30
| PRIOR PELLING DATE: 2004-06-30
| PRIOR PELLING DATE: 2004-06-30
| PRIOR PILING DATE: 2004-06-30
| PRIOR PILING DATE: 2004-06-30
| PRIOR PILING DATE: 2004-06-30
| NUMBER OF SEQ ID NOS: 2523
| SEQ ID NO 1571
| LENTH: 149
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OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying frui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
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                                                                             GKFEDMAKADKARYEREMKTYIPPKGETX----KKFKDPNAPKRPPSAFFLFCSEYRPKI 113
                                                                                                                                                                                114 KGEHP-GLSIGDVAKKLGEMWNYTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAK 172
                                                                                                                             GKSKGESKKAETKLAVNKKGAAATKGGKKPAKGKEPKDPNKPKRPPSAFFVFMADFREQY 63
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35.8%; Pred. No. 4.4e-13;
tive 29; Mismatches 54; Indels
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-----NKKLEGKDDEEGSDKSKSEVNDEDEDEDEEDEEDEDDD 149
                                                                                                                                                                                                                                                                                  173 KGVVKAEKSKKKKEEEEDEEDEEDEEBEEEEDEEDBDD 214
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LOCATION: (1)._(149)
OTHER INFORMATION: Public GI no. 729737
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Best Local Similarity 35.8
Matches 58; Conservative
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NAME/KEY: misc_feature
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LOCATION:
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Search completed: April 6, 2006, 10:33:30 Job time : 26.875 secs

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6, 2006, 10:33:08 ; Search time 189 Seconds (without alignments) 499.822 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 MGKGDPKKPRGKMSSYAFFV..........DEEEEEDEEDEDEEEDDDDE 215 2443163 segs, 439378781 residues Gapop 60.0 , Gapext 60.0 US-10-717-984-1 OLIGO Perfect score: Scoring table: Sequence: Searched: ritle:

2442881 Total number of hits satisfying chosen parameters:

Word size

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp1980s:* geneseqp2001s:* geneseqp2005s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human amp PRO polyp Human hig Human HMG pro hig hig hig aci Pro Pro Pro Pro Tumour-as Amphoteri Protein Human Human Human Human Human Human Amino Human Human Ado25918 Ado71477 Ado71477 Adox 4522 Adox 69343 Adox 6934 Abu07499 Ade57980 ADX69343 ADY14248 ADY85326 ADO25918 ADO71477 ADR45922 ABM81508 ABM85677 ADO60491 ADY85085 ADZ80804 ADE60447 Query Match Length DB 0.001 100.0 10 Score 222209876543210987654 222209876543210 Result

Abp64829 Human pro Abb57220 Mouse isc Aae35860 Mouse and Add47643 Rat Prote		Mous Huma Rat Rat		Ay73828 Human pro Ada55380 Human pro Aca90125 Human hig Abm81641 Tumour-as Ady85029 Rat and m
5 ABP64829 5 ABB57220 5 AAE35860 7 ADD47643	3 ADO25919 3 ADO71478 3 ADR87104 9 ADY85327	7 ABM85676 9 ADY85016 7 ADE60730 7 ADE57978		2 AAY73828 6 ADA55380 9 AEA90125 8 ABM81641 9 ADY85029
229 215 215 215 215	215 215 215 215 215	252 252 214 214		152 176 215 168 215
10 97.7 88 87.4 88 87.4 88			87 87.0 87 87.0 87 87.0 56 72.6	150 69.8 147 68.4 137 63.7 127 59.1 121 56.3
	29 30 31 11	333	33 33 39 40 11 11	44444 40244 6443

ALIGNMENTS

RESULT 1

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring. expression; differential regulation; Protein differentially regulated in prostate cancer #102. ABU07499 standard; protein; 215 AA (ORIG-) ORIGENE TECHNOLOGIES INC. 06-APR-2001; 2001US-0281732P. 08-APR-2002; 2002WO-US010824 06-APR-2001; 2001US-0281731P (first entry) WO200281638-A2. Jay G; Homo sapiens 28-JAN-2003 17-OCT-2002. ABU07499; Sun Z,

Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

WPI; 2003-058520/05. N-PSDB; ABX10404.

Claim 1; Page 413-414; 416pp; English

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer.

Human Human

Amino

Ade60728 Ads17580 Ady85051

ADE60728 ADS17580 ADY85051

ADE57984 ADE60732

Human

Ade60732

binding motif (HMG1 A box)"

/note= "DNA

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Treterably, une explaint that a case, to gain, an explaint of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially regulated cancer cells, which involves contacting a polypeptide differentially regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulates the biological activity (I) is useful as molecular markers, as drug targets, and for detecring, (I) preventing or treating, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic, the nature of genetic defect, etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide and thus for searching specific binding partners of the polypeptide and thus for specific genes, and groups of genes, expressed in pathways (I) in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways which are useful in diagnostic, therapeutic, and clinically continued and disease pathways and the delineations of targets in these applications. This is the amino acid sequence of a protein differentially
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Preferably, the expression levels of at least 10 genes are determined
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Matches 215; Conserv
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IID AAE3

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XX XX II7----

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The invention relates to high mobility group (HMG) protein comprising DNA binding motifes termed HMG A box and HMG B box. HMG A box or a non-chain motifes termed HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, peptic or duodenal ulcers, Crohn's classe, pronchitis, emphysema, HIV infection, candidisais, malaria, filariasis, amoebiaais, dermatitis, atherosclerosis, Alzheimer's disease, myocardiis, myocardial ischaemia, meningitis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpasture's asyndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMGI (also termed as HMGBI)
                                                                                                                                                                                                                                                                                                                               New isolated polypeptide having a vertebrate HWG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.
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                               binding motif (HMG1 B box)"
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               89. .162
/note= "DNA
                                                                                                                                  15-MAY-2002; 2002WO-US015329.
                                                                                                                                                                   15-MAY-2001; 2001US-0291034P.
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UNIV PITTSBURGH.
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Best Local Similarity 100.
Matches 215; Conservative
                                                                                                                                                                                                                                                                   Yang H,
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(UYPI-)
                                                                                                                                                                                                     (NSHO-)
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ADD40788 standard; protein; 215

ADD40788

disease;

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This invention describes a novel method comprising using high mobility group B proteins (HMGB) as target molecules for development or group B proteins (HMGB) as target molecules for development or compositions (compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention care used in kit for characterising the status of the endometrium, cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor Cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor Cycle and cytostatic activity. HMGB is part of a nuclear transcription factor complex and, extracellularly, a ligand for nuclear transcription factor complex and, extracellularly, a ligand for involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometriosis or polyps, hyperplasia or carcinoma of the endometrium, also contraceptives and methods for assessing status of the complex contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptives and methods for assessing status of the invention contraceptines.
                                                                                   high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease, contraceptive; endometrium; pregnancy; menstrual cycle irregularity; RAGE; receptor for advanced glycation end; gynaecological; cytostatic; nuclear transcription factor complex; tumour metastasis; endometriosis; polyps; hyperplasia; carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Developing treatment and diagnosis of endometrial disorders, using mobility group B proteins, or related nucleic acid or interaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2001; 2001DE-01062556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALCE-) ALCEDO BIOTECH GMBH.
                                   Human HMGB1 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                partners, as targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-505462/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bullerdiek J;
                                                                                                                                                                                                                                                                                Homo sapiens
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ö EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120 9 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF Gaps .. 0 Length 215; 0; Indels 100.0%; Score 215; DB 7; L 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0; SKKKKEEEEDEEDEEDEEBEEBEBBBBEEBDDDB 215 SKKKKEEEEDBEDEEDEEBEEBEBEBEBEDBDDE 215 Query Match 100. Best Local Similarity 100. Matches 215; Conservative 61 61 121 121 181 셤 8 ઠે 셤 ò 용 ò

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group B proteins (HMGB) as target molecules for development or preparation of compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention are used in kit for characterising the status of the endometrium, especially for presence of pregnancy or irregularities in the menstrual order. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor for advanced glycation end products). The products of the invention have synaecological, contraceptive and cytostatic activity. HMGB is part of a nuclear transcription factor complex and, extracellularly, a ligand for the surface RAGE (receptor for advanced glycation end products) which is involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometricals or polypes, hyperplasia or carcinoma of the endometrium, also contraceptives and methods for assessing status of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endometrium, particularly for detecting pregnancy or menstrual disorders.
This sequence represents the human HMGB1 protein used in the method of
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                                                                                                                                     endometrial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developing treatment and diagnosis of endometrial disorders, using high mobility group B proteins, or related nucleic acid or interaction
                                                                                                                                                       contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
nuclear transcription factor complex; tumour metastasis; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method comprising using high mobility
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                                                                                                                                     protein; HMGB1; HMGB2; HMGB3;
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                                                                                                                                                                                                                   carcinoma
                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2002; 2002WO-EP014579.
                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2001; 2001DE-01062556
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                                                                                                                                   group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          partners, as targets.
                                                                                                                                                                                                                 polyps; hyperplasia;
                                                                                            Human HMGB1 protein.
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Matches 215; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-505462/.
N-PSDB; ADD40787.
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                                                                                                                                                                                                                                                                                             WO2003051383-A2.
                                                                                                                                   mobility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bullerdiek J;
                                                                                                                                                                                                                                                          Homo sapiens.
                                                     15-JAN-2004
                                                                                                                                                                                                                                                                                                                                      26-JUN-2003.
                  ADD40788;
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15-JUL-2004 (first entry)
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                                                                                                                                                                                                                                                                                           JP2004107260-A.
                                                                                                                                                                                                                                                                   Homo sapiens
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 121
                                                                                                                                 ADO60491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel DNA and protein sequences which ser associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (ix) for diagnosing carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as markers of carcinoma including lymphoma. The present sequence is one such CAP. Note: This patent is an equivalent to basic patent US2002182586AI, for which no sequence data was published
SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
            SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
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                                               215
                                                            SKKKKEEEEDEEDEEDEEDEEDEEDEEDEEDEDDDB 215
                                                                                                                                                                                                                               Cytostatic; carcinoma; lymphoma; cancer; human.
                                              SKKKKEEEEDEEDEEDEEDEDEEDEDDDE
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                                                                                                                              ABM85677 standard; protein; 215
                                                                                                                                                                                                      Human protein sequence hCP43793.
                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                                             28-FEB-2003; 2003WO-US006235
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ses 215; Conservative
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                                                                                                                                                                                                                                                                            WO2003073826-A2
                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                     12-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                    Morris DW;
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                                                                                                                                                       ABM85677;
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This invention relates to a novel vaccine for promoting amyloid beta 42 aggregation inhibitory effect and/or amyloid beta 42 phagocytosis by microglia, which comprises a high mobility group protein 1 (HMGI), its partial peptide, or its salt. The invention may be useful for the production of compounds with a nootropic or neuroprotective activity acting as promoters of inhibition of amyloid beta 42 aggregation or promoters of amyloid beta 42 phagocytosis by microglia. The invention may also be useful for the production of a vaccine. The invention is useful for prophylaxis and/or treatment of Down's syndrome or amyloid angiopathy or preventing brain amyloidosis such as Alzheimer's disease. The present sequence is that of the protein encoded by the human high mobility group protein 1 (HMGI) gene which may be used during the creation of the novel
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SIGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; amyloid beta 42 aggregation; amyloid beta 42 phagocytosis; microglia; high mobility group protein 1; HMG1; nootropic; neuroprotective; microglia; vaccine; Down's syndrome; amyloid angiopathy; brain amyloidosis; Alzheimer's disease; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human high mobility group protein 1 (HMG1) protein SeqID2.
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100.0%; Pred. No. 8.2e-195;
ive 0; Mismatches 0;
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                                   SIGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
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SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine; pharmaceutical composition;
HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity.
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to one. B proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMP biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high mobility group box 1; HWGB1; HWGB A box; HWGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine ascade, sepsis; allograft rejection; rheumatord arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancratitis; reperfusion ischaemia; ashheri schaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
                        New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence
SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
                                                                                                                                                                                                                                                                                                                                                                                              Human high mobility group box 1 (HMGB1) protein #1
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20-NOV-2002; 2002US-0427846P.
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Matches 215; Conservative

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(proliferative) diabetic retinopathy, diabetic nephropathy, macular
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Matches 215;
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human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of nucleic acids encoding basic DNA-binding proteins, and their translation or transcription products, for treating diseases associated with e.g. angiogenesis, neovascularization or wound healing, also for
                                                                                                                              MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                          1 MGKGDPKKPRGKMSSYAPPVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                      Length 215;
                                                                              Indels
represents a human HMGB1 polypeptide of the invention.
                                                     Score 215; DB 8; I
Pred. No. 8.2e-195;
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2003DE-01010160.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                 Query Match
Best Local Similarity 100.
Matches 215; Conservative
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                          Sequence 215 AA;
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07-MAR-2003;
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degeneration, arthritis, endometriosis, histiocytosis, psoriasis, rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma, Raposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis, angina pectoris, ischaemia, infarction, infertility, wounds (including diabetic and other ulcers), also diseases associated with DNA damage, especially xeroderma pigmentosum, leather skin', skin cancers and ageing (including where associated with sunburn) and cardiac infarct, including cosmetic treatment, especially as a sun-protection composition. Compounds identified as modulators of the specified processes can also be used
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                                                                                                                                                                                                                                   therapeutically. The present sequence is a protein of the invention.
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                                                                   Delypeptides, and their related nucleic ascids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide perfective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide of card and antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central necrosed system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                          The invention relates to human tumour-associated antigenic target (TAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 215;
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 215; DB 8; L 100.0%; Pred. No. 8.2e-195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                            Claim 12; SEQ ID NO 3888; 7273pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 215; Conservative
 cancer or tumor,
                                                                                                                                                                                                                                                                                                                                                                                Sequence 215 AA;
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The present invention relates to new vascular endothelial growth factor (VEGF) proteins useful for skin healing of a skin graft onto underlying tissue. The method involves contacting a skin graft/flap or underlying tissue with an agent chosen from vascular endothelial growth factor C (VEGF-C) polymucleotides, vEGF-C polymeptides, VEGF-D polymucleotides, or amount effective to reduce edema or increase perfusion at skin graft or flap. The composition comprises a gene therapy vector that encodes VEGF-C polymotleotide. The VEGF-C polympeptides are therapy vector that encodes VEGF-2 polymotleotides. The VEGF-C polympeptides are therapy vector that encodes VEGF-3 ligand amino acid sequence chosen from a prepro-VEGF-C sequence, and fragments that binds VEGF-3, where Z comprises a heparin-binding amino acid sequence, and B comprises a comprises a heparin-binding amino acid sequence, and B comprises a comprises a heparin-binding amino acid sequence, and B comprises a comprise will be set to be sequence, and VEGF-D polympetides, VEGF-C polymotleotides, vEGF-C polympetides, VEGF-D polymotleotides, and VEGF-D polympetides, vEGF-C polymotleotides, and vEGF-C polympetides, vEGF-C polymotleotides, and vEGF-D polympetides or vEGF homology domain (VHD) and a heparin-binding domain. Vulnerary. Gene vEGF homology domain (VHD) and a heparin-binding domain. Vulnerary is breast are constructive surgery. The reconstructive surgery, a liposuction procedure, or skin cancer, skin grafts, cosmetic surgery and improves complications resulting from surgery which includes excessive bleeding, such as hematomas, bruising and wound-healing difficulties, pain, edema, necrosis and technial general requence is amphoterin protein, which contains a heparin binding domain related to the invention.
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                                                                                                                                                                                                                                        Asko-Seljavaara S;
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                                                                                                                                                                                                                                        Tammela T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
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                                                                                                                                                                                                                                        Karkkainen M,
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                                                                                                               (LICW) LICENTIA LTD.
12-JUN-2003; 2003US-0478114P.
12-JUN-2003; 2003US-0478390P.
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Matches 215; Conservative
                                                                                                                                                                                                                                   Saaristo A,
a S, He Y;
                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-142834/15.
                                                                                                                                                                                                                                                                     Yla-Herttuala S,
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(first entry)

05-MAY-2005

(first entry)

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ADY14248 standard; protein; 215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to heparin-binding vascular endothelial growth factor receptor 3 (VEGRR-3) proteins and encoding polynucleotides. The heparin binding VEGRR-3 proteins are used for stimulating lymphangiogenesis or angiogenesis in a mammal, and for modulating the growth of mammalian endothelial cells, mammalian endothelial precursor cells or hematopoictic progenitor cells. The polypeptide may also be used for promoting recruitment, proliferation, differentiation, migration or survival of neuronal cells or neuronal precursor cells, and for treating neurodegenerative disorder, e.g. Alzheimer's diseases, Parkinson's disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral Sclerosis (ALS), dementia, or cerebral palsy. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                              New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                   amphoterin; Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian; Anticonvulsant; VEGF-3 receptor; Anglogenesis stimulator; Gene Therapy; vascular endothelial growth factor receptor 3; VEGFR-3; anglogenesis disorder; neurodegenerative disorder; Alzheimers disease; anglogenesis disease; motor neurone disease; dementia; paralysis; VEGF-C; neurological disease; Huntingtons chorea; vascular endothelial growth factor receptor 3; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 63; 219pp; English.
                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                        12-JUN-2003; 2003US-0478390P. 23-SEP-2003; 2003US-00669176.
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                                                                                                                                                                                                                                                                                                                                                                                         Tammela T;
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Les 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huntington's disease
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
                                                    Antinflammatory; Immune disorder; Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; diagnosis.
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100.0%; Score 215; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0; Indels
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polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
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Length 215; Indels

100.0%; Score 215; DB 9; I 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 215; Conservative

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EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

61 61 121

1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHDDASVNFSEFSKKCSERWKTWSAKEKGKF

1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF

121 SIGDVAKKLGEMWNYTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

215

181 SKKKKEEEEDEEDEEDEEEEEDEEDEEDEEDDDD 215 SKKKKEEEEDEEDEEDEEEEEDEDEDEE

181

SIGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK

(first entry)

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02-JUN-2005
ADY85326;
       Region
        Region
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High mobility group box; HWGB1; immune disorder; infection; immunosuppressive; autoimmune disease; allergy; antiallergic; ulcertative colitis; antiaflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiathmatic; rethematoid arthritis; antirheumatic; antiathritis; antirheumatic; antiappressis; antipporiatic; systemic lupus erythematosus; dermatological; antiulcer. Human high mobility group box protein HMGB1. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES Location/Qualifiers 32. .85 /label= A_box /label= B_box 10-SEP-2004; 2004WO-US029540 10-SEP-2003; 2003US-0502349P. (GEHO) GEN HOSPITAL CORP .161 Warren HS, Tracey KJ; WPI; 2005-233421/24. WO2005025604-A2 Homo sapiens 24-MAR-2005

Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment.

Claim 6; SEQ ID NO 1; 57pp; English.

The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural HMGB A box. The immune pathology is induced by the administration of a non-human antigen, non-self material (e.g. a cell or tissue such as bone marrow cells) or adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of individual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune response to an administered non-human antisen comprise administering a HMGB A box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of the vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate in an individual comprises administering a wertebrate HMGB A box, or an immunosuppressive fragment or non-naturally-occurring HMGB A box, or an immunosuppressive administering a mann-naturally-occurring HMGB A box, or an immunosuppressive and a successive or non-naturally-occurring HMGB A box, or an immunosuppressive and a successive or non-naturally and a successive or non œ as the fragment of these, and a vertebrate or non-naturally-occurring HMGB is box. The HMGB polypeptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, psoriasis or systemic lupus erythematosus (all claimed). The present sequence is that of the human HMGBI protein, which can be used as the HMGB polypeptide in methods of the invention.

The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HWGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HWGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of Disclosure, SEQ ID NO 2; 123pp; English.

Sequence 215 AA;

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New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                                                             High mobility group box; HMGB1; monoclonal antibody; antibody therapy; sepsis, antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiathmatic; lupus erythematosus; antiinflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress; peritoric; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; garaft versus host disease; inflammatory bowel disease; asthmatory cachexis; anabolic; infection; musculoskeletal disease; immune disorder.
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                           ADY85085 standard; protein; 215
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                                                                                                                    Human HMGB1 A box.
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                                                          ADY85085;
RESULT 15
               ADY85085
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detecting an HMGB polypeptide in a sample. The antibody (or antigen-
binding fragment) binds to a vertebrate HMGB A box but does not
specifically bind to non-A box epitopes of HMGB, and inhibits release of
a proinflammatory cytokine from a vertebrate cell treated with an HMGB
protein. A method of treating a condition characterized by activation of
an inflammatory cytokine cascade comprises administering an antibody of
the invention, or its antigen-binding fragment. The condition is selected
from sepsis, allograft rejection, arthritis, asthma, lupus, adult
respiratory distress syndrome, chronic obstructive pulmonary disease,
psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
graft versus host disease inflammatory bowel disease, multiple sclerosis
and cachesia, especially sepsis, arthritis, or lupus. The present
sequence is that of the A box of human HMGB1 ADY855012. An identical
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Sequence 215 AA;

0; Gaps 100.0%; Score 215; DB 9; Length 215; 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0; Indels (Best Local Similarity 100. Matches 215; Conservative ò

9 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF

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completed: April 6, 2006, 10:36:45 Search co Job time

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model OM protein April Run on:

6, 2006, 10:37:03 ; Search time 41 Seconds
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US-10-717-984-1

215 1 MGKGDPKKPRGKMSSYAFFV......DEEEEEDEEDEEEDDDDE Perfect score:

Scoring table: Sequence:

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283416 segs, 96216763 residues Searched:

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

nonlistone chromos high mobility grou nonhistone chromos high-mobility grou nonhistone chromos hypothetical prote HWG-1 - chicken nonhistone chromos nonhistone chromos nonhistone chromos nonhistone chromos high-mobility-grou high mobility grou nonhistone chromos nonhistone chromos high mobility grou HMG1 protein homol nonhistone chromos troponin T - fruit high mobility grou nonhistone chromos non-histone chromo gene HMG-T2 protei troponin T - fruit dorsal switch prot nonhistone chromos nonhistone chromos Description SUMMARIES S02826 S01947 NSRTH1 14868 A27853 A28897 A24019 S44019 S48108 T01071 NSHUH2 A34719 SS4774 SS68823 SS68823 SS62355 SJ621129 JC11129 JC11129 JC1114 B61611 TA22953 ISC254 SS2359 SS2359 SS2359 SS2359 四 Length Query Result No.

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100.0%; Score 215; DB 2; Length 215; larity 100.0%; Pred. No. 1e-179; Conservative 0; Mismatches 0; Indels (

Query Match Best Local Similarity Matches 215; Conserv

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ALIGNMENTS

RESULT 1 S02836 Conditione chromosomal protein HMG-1 - human Conditione chromosomal protein HMG-1 - human Conditione chromosomal protein HMG-1 - human Conditione S02826; A33178; G33178 C;Accession: S02826; A33178; G33178 R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R. R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R. Ryden, L.; Huang, J.K.; 1197-1214, 1989 A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1. A;Reference number: S02826; MUID:89160247; PMID:2922262 A;Accession: S02826 A;Molecule type: mRNA A;Residues: 1-215 < WEN>
A;Cross-references: UNIPROT:PO3429; UNIPARC:UPI0000015ED; EMBL:X12597; NID:g32326; PIDN R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J. Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro A;Reference number: A33178; MUID:91176935; PMID:2079031 A;Accession: A33178 A;Molecule type: protein A;Residues: 2-13,'XXF' <war> A;Cross-references: UNIPARC:UP100001771D7 A;Accession: G33178 A;Molecule type: protein A;Residues: 2-13,'XX',16-22 <wa2> A;Cross-references: UNIPARC:UP100001771D7 C;Genetics: A;Cross-references: UNIPARC:UP100001771D7 C;Genetics: A;Cross-references: GDB:133789; OMIM:163905 A;Map position: 13q12-13q12</wa2></war>
C;Superfamily; nonhistone chromosomal protein HWG-2; HWG box homology C;Keywords: chromosomal protein; DNA binding; nucleus F;6-83/Domain: HWG box homology <hwg1> F;92-166/Domain: HWG box homology <hwg2></hwg2></hwg1>

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Thu Apr

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nonhistone chromosomal protein HMG-1 - rat
N'Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A41175; A27299; A30188; B48771; A48771; C48771
R;Mercmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
J. Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-Kba heparin-binding protein of brain (amphoterin) involved in neurite outgro
A;Reference number: A41175; MUID:91358468; PMID:1885601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN::
A;Note: part of this sequence, including the amino end of the mature protein, was confirm
A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
h-mobility group proteins
R;Paonessa, G.; Frank, R.; Cortese, R.
R;Paonessa, G.; Frank, R.; Cortese, R.
A;Title: Nucleotide sequence of rat liver HMG1 cDNA.
A;Reference number: A27298; MUID:88067717; PMID:3684582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A27298
A;Molecule type: mRNA
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>
A;Cross-references: UNIPARC:UP10000173984
B;Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P. J. Cell Biol. 107, 2293-2305, 1988
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Parkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvala, B. Baol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced a A;Reference number: A48771; MUID:93374971; PMID:8366113
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A.Molecule type: protein
A.Status: 98-105./x', 107-112 <PA2>
A.Molecule type: protein
A.Status: 98-105./x', 107-112 <PA2>
A.Cross-references: UNIPARC:UPI0000173986
A.Experimental source: postnatal brain
A.Note: sequence extracted from NUSI backbone (NCBIP:137788)
C.Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C.Reywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental
F;6-83/Domain: HMG box homology cHMG1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.4%; Score 188; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.3e-156;
Matches 188; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC:UP10000173985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-215 <MER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A41175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A30188
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                                                                                                                                                                                                                                                                          Nothistone chromosomal protein HWG-1 - bovine
NyAlternate names: 33K protein; high-mobility-group protein HMG-1
C;0species: Bos ptimigenius taurus (Cattle)
C;0ate: 30-8ep-1899 #sequence revision 22-Apr-1995 #text_change 09-Jul-2004
C;0ate: 30-8ep-1899 #sequence revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; A61611; S10559; 145910
R;Kaplan, D.J.; buncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Accession: S01947
A;Molecule type: mRNA
A;Reference number: S01947; MUD:89057489; PMID:3194213
A;Molecule type: MNA
A;Residues: 1-21s - KAAP
A;Cross-references: UNIPROT:P10103; UNIPARC:UP1000016C31D; EMBL:X12796; NID:9416; PIDN:C
R;Malker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FBBS Lett. 122, 264-270, 1980
A;Tefle: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUD:81138848; PMID:7202717
A;Accession: A61611
A;Accession: A61
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A/Rocession: S10959
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A/Rocession: S10959
A/Rocession: S10959
A/Rocession: S2-2, x' x',24-38 cCRR>
A/COSS references: UNIPARC:UF10000173989
B/Sentecost, B.T.; Dixon, G.H.
A/Rocession: 145910; MUID:84128872; PMID:6141822
A/Rocession: 145910; MUID:84128872; PMID:6141822
A/Rocession: 145910; MUID:84128872; PMID:6141822
A/Rocession: 145910
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Rocession: 165910
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Rocession: 165910
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Rocession: 165910
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Rocession: 16504, 113, v', 121-215 cERN
A/Rocession: 16504, 113, v', 121-215 cER
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SKKKKEEEEDEEDEEDEEDEEDEEDEDDDE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKKKKEEEEDEEDEEDEEDE 206
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Matches 206; Conservative
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A; Molecule type: mRNA
A; Residues: 1-215 <TSU>
A; Residues: 1-215 <TSU>
A; Cross-references: UNIPROT: P12682; UNIPARC: UPI000016C6C4; GB: M21683; GB: M21684; NID: g16
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords: chromosomal protein; DNA binding; nucleus
P; 6-83/Domain: HMG box homology <HMG1>
F; 92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 120
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C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                              1 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF
                                                                                                                                                                                                                                                                                                                                                                                                CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK
                                                                                                                                                                                                                                                                               46 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF
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               C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DMA binding; nucleus F:1-38,Domain: HMG box homology (fragment) <HMG1> F:47-121/Domain: HMG box homology <HMG2>
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R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
                                                                                                                                                           Length 170;
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R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, P.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 x
A;Reference number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
                                                                                                                                                              Score 143; DB 2; Le
Pred. No. 4.1e-117;
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Pred. No. 2.7e-115;
                                                                                                                                                                                       ilarity 100.0%; Pred. No. 4.1
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKPDAAKKGVVKAEKSKKKEEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 GKPDAAKKGVVKAEKSKKKKEEE 188
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                                                                                                                                                           66.58;
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A: Residues: 1-216 <STR>
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Best Local Simi
Matches 143;
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non-histone chromosomal high-mobility group 1 protein - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148689; A55402; I57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Fitle: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Reference number: 148688
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-215 cRRS
A;Cross-references: UNIPROT:P07155; UNIPRAC:UP100000008A6; EMBL:Z11997; NID:953381; PIDN R;Perrari, S:; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J; Biol. Chem. 269, 28803-28808, 1994
A;Ritle: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402; MUID:95050689; PMID:7951836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary; not compared with conceptual translation
Modecule type: DNA
A;Residues: 1-189, 191-215 <FER>
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
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nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
(.)Species Cricetulus griseus (Chinese hamster)
(.)Species Cricetulus griseus (Chinese hamster)
(.)Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
(.)Accession: A27853
Kilee, K.L.D.; Pentecors, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: mRNA
A;Residues: 1-170 <LEE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
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Mamm. Genome 5, 91-99, 1994
A.Title: Wolecular cloning expression analysis, and chromosomal localization of
A.Reference number: IS7021; MUID:94235965; PMID:8180479
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 100.0
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-215 <RE2>
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high mobility group protein T - rainbow trout
NiAlternate names: HMG-T protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Accession: T01071
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high A;Reference number: A24019; MUID:85269614; PMID:4022777
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A,Accession: A42425
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Rolecule type: DNI
B,Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
A,Title: Sequence of human HMG2 cDNA
A,Title: Sequence of human HMG2 cDNA
A,Reference number: S20061; MUID:92093633; PMID:1754403
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A;Molecule type: mRNA
A;Rossidues: 1-209 <MAJ>
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
C;Genetics:
A;Gene: GBB:NHCP2
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C;Dacession: A4425; Bsoudence revision 31-Mar-1992 #text_change 09-Jul-2004
C;Dacession: A4425; S20061; S18068
R;Shirakawa, H.; Yoshida, M.
J. Biol. Chem. 267, 6641-6645, 1992
J. Biol. Chem. 267, 6641-6645, 1992
A;Fitle: Structure of a gene coding for human HMG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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8.2e-18;
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A;Molecule type: mRNA
A;Residues: 1-204 <PEN>
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100.0%; Preq. ...
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Matches 26; Conservative 0; Mismatches
           33 ASVNFSEFSKKCSERWKTMSAKEKGKFED 61
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C.Species: Salmo sp. (trout)
C.Species: Salmo sp. 
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548708
high-mobility-group-1 protein - trout
high-mobility-group-1 protein - trout
C;Species: Salmo sp. (trout)
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708
By Stros M.; Nishikawa, S.; Dixon, G.H.
Bur. J. Biochem. 225, 581-591, 1994
A;Title: cDNA sequence and structure of a gene encoding trout testis high-mobility-group
A;Reference number: S48708; MUID:95045507; PMID:7957172
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                                                                                                                                                                                                                                                                                                                                                                                 PSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKD 158
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-204 «STR>
A.Cross-references: UNIPARC:UDIO0001771D9
C.Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F.5-82/Domain: HMG box homology «HMG2»
F.91-165/Domain: HMG box homology «HMG2»
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                                                                                                                                                                                                                                 Length 216;
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Pred. No. 7.1e-18;
                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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A24019
nonhistone chromosomal protein HMG-T - trout (fragment)
                                                                                                                                                                                                                             Query Match
50.2%; Score 108; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.5%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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Matches 29; Conserval
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Best Local Similarity
Matches 29; Conserva
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Length 54; Indels

DB 2; Le 6.3e-14;

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R;Stolzenburg, F.; Dinkl, B.; Grummt, F. Nucleic Acids Res. 20, 4927, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the non-histone chromosomal high m. A;Reference number: I48408; MUID:93027215; PMID:1408807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross.references: UNIPROT:P30681; UNIPARC:UPI00016CDD8; EMBL:X67668; NID:g51338; PIDN A;Note: this is a revision to the sequence from reference $25487
R;Stolzenburg, F.; Dinkl, E.; Grummt, F.
submitted to the EMBL Data Library, August 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-183, KNUSED',190-195,'E',197-198,'ED',201-202,'G',204-205,'EDEE' <STW>
A;Cross-references: UNIPARC:UPI00001771D1; EMBL:X67668
A;Note: this sequence has been revised in reference S26062
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Date: 11-Mar-1998 #sequence revision 17-Apr-1998 #text_change 09-Jul-2004
C.Accession: S26062; S25487; I48408
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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F;6-54/Domain: HMG box homology #status atypical <HMG>
                                                                                                                                                                                                                                                                                                                                                                                                        nonhistone chromosomal protein HMG-2 - mouse N;Alternate names: high mobility group 2 protein C;Species: Mus musculus (house mouse)
                                                       Query Match 11.2%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 6.3 Matches 24; Conservative 0; Mismatches
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                                                                                                                                                                                     28 KKKHPDASVNFSEFSKKCSERWKT
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A; Residues: 1-205 <STO>
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                         A34719

nonhistone chromosomal protein HMG-2 - pig
C;Species us scrofa domestica (domestic pig)
C;Species us scrofa domestica (domestic pig)
C;Date: 06-U1-1990 #sequence_revision 06-U1-1990 #text_change 09-U1-2004
C;Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle
A;Reference number: A34719; MUID:90275208; PMID:2350545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P30681; UNIPARC:UP1000016432C; EMBL:Z46757; NID:g609168; PID C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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A; Residues: 1-210 <SHI>
A; Residues: 1-210 <SHI>
A; Residues: 1-210 <SHIS
Cross-references: UNIPARC: UNIPARC: UPI000016C6C5; GB:J02895; NID:g164491; PIDN: C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords: chromosomal protein; DNA binding; nucleus
F; 6-83/Domain: HMG box homology <HMG1>
F; 92-166/Domain: HMG box homology <HMG2>
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S54774
high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S5211
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of
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A;Experimental source: C44 MEL cells
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
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A;Status: preliminary; nucleic acid sequence not shown
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Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                A; Accession: A34719
A; Status: preliminary
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Matches
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S68823
   RESULT 12
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homo sapien

brachydanio brachydanio oncorhynchu homo sapien mus musculu

homo sapien

xenopus tro xenopus lae mus musculu

mus musculu

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High-mobility group box 1.

Name=HMGBL; ORENames=RP1L-550P23.1-004;
Homo sapiens (Human).

Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
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04R8447
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Testis cDNA clone: QtsA-13487, similar to human high-mobility group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL353648; CAIIS600.1; -; Genomic_DNA.
GO; GO:0000785; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 215; DB 2; Length 215; 100.0%; Pred. No. 1.2e-184; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pelan S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Q9CT19 MOUSE
Q96J53 HUMAN
                                                                Q80YZ1_MOUSE
Q9NQJ4_HUMAN
HMG2_BOVIN
Q7TPS2_MOUSE
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QSBKQ1 1
Q9NYD7 1
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01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
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NUCLEOTIDE SEQUENCE.
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Matches 215; Conserv
12.55
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NCBI_TaxID=9606;
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1D Q4R844 MA
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DT 13-SEP-20
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canis famil
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656.661 Million cell updates/sec
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O5t7c5
O9dwy6
O548r9
Q58ev5
P63158
P63159
Q8bnm0
Q8c7c4
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09puk9
09yh06
                                                                                                                     2006, 10:33:48 ; Search time 231 Seconds
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Q6yka4
P09429
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                   GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                                                                          2166443 seqs, 705528306 residues
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04R844_MACFA
HMC1_CANPA
HMC1_HUMAN
HMC1_BOVIN
0517Č5_HUMAN
0577Č5_HUMAN
0548P8_RAT
058BV5_WOUSE
HMC1_MOUSE
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Q8C7C4 MOUSE
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OST7C4 HUMAN
OS9GW1 HUMAN
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OST7C6 HUMAN
O88611 SPAEH
HMG1 PIG
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Q5T7C1 HUMAN
Q88612 SPAEH
Q6P202 MOUSE
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Q8BQ02_MOUSE
HMG1X_HUMAN
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Q9PUK9_CHICK
Q9YH06_CHICK
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                                                                                   protein search, using sw model
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Match Length DB
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Score

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Word size

Perfect score:

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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01-WAR-1989 (Rel. 10, Created)
01-AUG-1990 (Rel. 15, Last aunotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;
The active gene that encodes human high mobility group 1 protein (HMG1) contains introns and maps to chromosome 13.";
Genomics 35:367-371(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA].
MEDLINES 89160247; PubMed=2922262;
Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
"A human placental cDNA clone that encodes nonhistone chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 Asp/Glu-rich (acidic).
24763 MW; B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%; Score 214; DB 1; Le 100.0%; Pred. No. 9.7e-184;
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                                                                                           EMBL; AY135519; AAN11296.1; -; mRNA.
EMBL; AY13521; AAN1319.1; -; Genomic_DNA.
HSSP; PO7145; 1AAB.
ENSEW, OGYKA4; 1-83, 92-170.
Ensewbl; ENSCAFGO000006597; Canis familiaris.
InterPro; IPRO00135; Highmoblty_12.
InterPro; IPRO00915; Highmoblty_12.
Pfam; PF00505; HMG_box; 2.
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Nucleic Acids Res. 17:1197-1214(1989),
                                                                                                                                                                                                                                                                                        PRINTS; PR00886; HIGHMOBLTY12.
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COMPBIAS
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                            International consortium for macaque cDNA sequencing, analysis, "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications."; submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last amoutation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercoplithecidae; Cercoplithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                        Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Habhimoto K.; Subanitution rate and structural divergence of 5.UTR evolution: Comparative analysis between human and cynomolgus monkey coDAS."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AB166615; BAE00728.1; -; mRNA. SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Les 215; Conservative
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1 (HMGB1),.
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HMG1_CANFA
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REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSPERS R.L., Feingold E.A., Grouse L.M., Derge J.G.,

RIAUSNER R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.R.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RADACHORO, L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.A., McGwan P.G., Peters G.J., Abramson R.D., Mullahy S.J.,

Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McGwan P.C., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radan A., Touchman J.W., Green E.D., Dickson M.C.,

Radiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Rochnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rocheration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

"Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201).";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
Simpson R.M., Ji H., Eddes J.S.,
Simpson R.J., Dorow D.S.;
Two-dimensional electrophoretic analysis of human breast carcinoma proteins: mapping of proteins that bind to the SH3 domain of mixed lineage kinase MLK2.";
Electrophoresis 18:588-598(1997).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S. Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y. Phelan M., Farmer A.;

"Cloning of human full-length CDSs in BD Creator(TM) system donor
                                                  He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P04637:TP53; NDExp=1; IntAct=EBI-389432, EBI-366083; 015350:TP73; NDExp=1; IntAct=EBI-389432, EBI-389606; SUBCELLUIAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the HMG1/HMG2 protein family. SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                          TISSUE=Small intestine;
The German cDNA consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [LARGE SCALE MRNA].
                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 57-64 AND 112-126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Mammary carcinoma;
MEDLINE=97295304; PubMed=9150946;
[3]
NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."
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121 IGDVAKKIGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180
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IDA.
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1-MG-1999 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                   R GO; GO:0000793; C:condensed chromosome; IDA.
R GO; GO:00008301; F:DNA bending activity; TAS.
R GO; GO:0008134; F:transcription factor binding; TAS.
GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.
GO; GO:0006281; P:DNA recombination; TAS.
R GO; GO:0006281; P:DNA repair; TAS.
R GO; GO:0006282; P:DNA unwinding; NAS.
R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R InterPro; IPR000135; Highmoblty_12.
R InterPro; IPR000101; HMG_Dox; Z.
R Ffam; PF00505; HMG_Dox; Z.
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PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; Direct protein sequencing; DNA-binding;
Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%; Score 214; DB 1; Length 214; 100.0%; Pred. No. 9.7e-184; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMG box 1.

HMG box 2.

Asp/Glu-rich (acidic).
E - D (in Ref. 5).

B 32GA80FC7P0F433 CRC64;
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                                                                                                                                                                                                                                                                                    IntAct; P09429; -.
Ensembl; ENSG0000189403; Homo sapiens
                                                                  -; mRNA.
-; mRNA.
-; mRNA.
-; mRNA.
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AY377859; AAQ91389-1;
CR749614; CAH18408-1;
CR7456863; CAG33144-1;
BT0006940; AAP35586-1;
BT000159; AAA93961-1;
BC003378; AAH03378-1;
BC0030981; AAH03378-1;
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                                                                                                                                                                  BC066889; AAH66889.1;
BC067732; AAH67732.1;
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Matches 214; Conservative
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                                                                                                                                                                                                                                                                                                                                     HGNC; HGNC: 4983; HMGB1.
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                                                                                                                                                                                                                 PIR; S02826; S02826
HSSP; P07156; 1NHN.
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P10103;
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ID HMG1_BC
AC P10103;
DT 01-MAR
DT 13-SEP-
DE High mc
                             EMBL;
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EMBL;
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120 121

19 9 181

EMBL; X12597; CAA31110.1; -; mRNA.

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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
MEDLINE-81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;
Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
"The primary structures of non-histone chromosomal proteins HMG 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6; Christen T. Bischoff M., Hobi R., Kuenzle C.C.; Christen T., Bischoff M., Hobi R., Kuenzle C.C.; Christen T., Bischoff M., Hobi R., Kuenzle C.C.; Christon T., Elschoff M., Hobi R., And 2 bind preferentially to brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not to other types of Z-DNA."; C-DNA."; C-DNA."
                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
MEDLINE=84128872; PubMed=6141822;
Pentecost B., Dixon G.H.,
Fontecost and partial sequence of bovine cDNA clones for the high-mobility-group protein (HMG-1).";
Biosci. Rep. 4:49-57(1984).
                                                                                                                                                                                                   Kaplan D.J., Duncan C.H.; "Full length conners sequence for bovine high mobility group 1 (HMG1)
                                  Bos taurus (Bovine).
Sukaryota, Metazos, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00353; HMG BOX_1; 1.
PROSITE; PS00353; HMG BOX_2; 2.
Chromosomal protein; Direct protein sequencing; DNA-binding;
Nuclear protein; Repeat.
INIT_MET
                                                                                                                                                                                                                                            protein.";
Nucleic Acids Res. 16:10375-10375(1988)
                                                                                                                                              NUCLEOTIDE SEQUENCE (MRNA).
STRAIN-Holstein, TISSUE-Fetal thymus;
MEDLINE-89057489; PubMed=3194213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X12796; CAA31284.1; -; mRNA.
EMBL; M26110; AAA30567.1; -; mRNA.
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PRINTS; PR00886; HIGHMOBLTY12.
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B1).
Name=HMGB1; Synonyms=HMG1;
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                                                                                                             NCBI_TaxID=9913;
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DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMR; Q5T7C5; 2-84, 93-171.

GO; GO:0000785; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG_12_box.
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                Length 214;
HMG box 1.
HMG box 2.
Asp/Glu-rich (acidic).
C -> S (in Ref. 3).
C -> A (in Ref. 3).
EHPGL -> PGGGV (in Ref. 2).
C -> h (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.3%; Score 192; DB 2; Length 192;
100.0%; Pred. No. 5e-164;
.ive 0; Mismatches 0; Indels
                162 HMG box 1.
164 ASP/Glu-rich (acidic).
22 C -> S (in Ref. 3).
20 C -> A (in Ref. 3).
219 EHPGL -> PGGGV (in Ref. 2).
22 B -> D (in Ref. 3).
23 E -> D (in Ref. 3).
24777 MW; B283A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL353648; CAI15602.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22050 MW; 6A52DB61DA307C1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FBB-2005 (TrEMBLrel. 29, Created)
01-FBB-2005 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment)
Name-HighSI; ORPMames-RPII-550P23.1-001;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                95.3%; Score 205; DB 1; Le
100.0%; Pred. No. 1.2e-175;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKKKEEEEDEEDEEDEEDE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 KKKKEEEEDEEDEEDEEDEEDE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000910; HMG 12 box. Pfam; PF00505; HMG box; Z. PRINTS; PR00086; HJGHWOBLTY12. SWART; SM00398; HMG; 2. PROSITE; PS00353; HMG BOX 1; 1. PROSITE; PS50118; HMG BOX 2; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QST7CS_HUMAN PRELIMINARY;
ID QST7CS_HUMAN PRELIMINARY;
AC QST7CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 192; Conservative
                                                                                                                                                                                                                                                                                         Local Similarity 100.
1es 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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STRAINE-EVBN N. TISSUE-Colon, and Mammary tumor. C3;

MEDLINE-22388257; Pubbed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

B Rownstein M.J. Usdin T.B., Formide M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
1419h mobility group box 1 (16 days neonate thymus cDNA, RIKEN full-
length enriched library, clone:A130064K11 product:high mobility group
box 1, full insert sequence) (13 days embryo heart cDNA, RIKEN full-
length enriched library, clone:D330050N16 product:high mobility group
box 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SIGDVAKKLGEMWINITAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                   nautus iudzvejztus (mat).
Bukaryota; Metazoa (Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus muscul.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.4%; Score 188; DB 2; Length 215; 100.0%; Pred. No. 2.2e-160; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Kidney;
Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
"Amphoterin is associated with the development of the ki
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR273734, AAR82799.1; -: mRNA.
SEQUENCE 215 AA; 24894 MW; 8A868DBZ66D552B5 CRC64;
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE PRELIMINARY;
                                                                                                                                                                             Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 188; Conservative
                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae, Murinae, Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKKKKEEE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKKKKEEE 188
                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                          NCBI_TaxID=10116;
                                       Amphoterin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Hmgb1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VS MOUSE
Q58EV5_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q58EV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q58EV5
       HAPPEN SERVICE STREET S
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SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                             SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEBEEDEEDE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTY I PPKGETK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee K.-L.D., Lum H.-K., Nevo E.;
Submitted (UUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AP078819; AAC27652.1; -; Genomic_DNA.
HSSP; P07156; INHN.
SMR; Q9QWY6; 2-84, 93-171.
SO, GO:000785; C:chromatin; IEA.
GO; GO:0005634; C:uchcleus; IEA.
GO; GO:0005634; C:uchcleus; IEA.
GO; GO:0006555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR0005010; HMG 12_box.
PREM; PF05055; HMG box; Z_box.
PREM; PF05055; HMG box; Z_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D20D659274B575B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 189; DB 2; Le
Pred. No. 2.7e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.9%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae; Spalacinae; Nannospalax, NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00353; HMG BOX 1; 1. PROSITE; PSS0118; HMG BOX 2; 2. SEQUENCE 215 AA; 24822 WW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00886; HIGHMOBLTY12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High mobility group protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQWY6 SPAEH PRELIMINARY;
QQQWY6;
                                                                                                                                                                                                                                                  SKKKKEEEEDEE 192
                                                                                                                                                                                                                                                                                          SKKKKEEEEDEE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 100.
189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00398; HMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEEEDDDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
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                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
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Best Local 8
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STRAING-STREAM A. Shibatat, and Thymus;

KATAING-STREAM A., Shibata K., Yoshino M., Itch M., Ishii Y.,

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kashkawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Rieischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullica M., Marioldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Whynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havachi J., V. NUCLECTIBE SEQUENCE.

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NUM Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butteffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Merra M.A., Generation and initial analysis of more than 15,000 full-length human STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999). Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. NIH MGC Project; Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). STRAIN=FVB/N; TISSUE=Mammary tumor. C3; and mouse cDNA sequences."; STRAIN=FVB/N; TISSUE=Colon; NIH MGC Project; Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE

CSTRAIN-CSTBL/61 TISSUE-Heart;
Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu W., Hiraoka T., Hirozane T., Hayashida K., Hayatsu W., Hiraoka T., Hirozane T., A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kojima Y., Konno H., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Konno H., Konno H., Koya S., Kurihara C., Mateuyama T., Miyazaki A., Murata M., Ohsato N., Osazaki Y., Saitoh H., Satoh H., Sakai C., Sakai C., Sakai K., Sakazume N., Sano H., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the EmBli/GenBank/DDBJ databases.

EMBL; BC091741; AA4917411; -; mRNA.

EMBL; AK037928; BAC3928021; -; mRNA.

EMBL; AK037928; BAC3928021; -; mRNA. STRAIN=C57BL/63; TISSUE=Heart, and Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furno M., Hanagaki T., Hara A., Hashizume W., Fukuda K., Harapaki T., Hara A., Hashizume W., Horis E., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Shizaki T., Sogabe Y., Tagami M., Tagami D., Shibate K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwke S., Inoue K., Togawa Y., Izawa M., Ohara B., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKE integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). GO:0005634; C:nucleus, TAS.
GO:0005634; C:nucleus, TAS.
GO:00130235; F:nitric-oxide synthase regulator activity; IDA.
GO:0005515; F:protein binding; IPI.
GO:0005819; P:protein binding; IPI.
GO:0006810; P:transport; IDA. Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., GO; GO:0005615; C:extracellular space; IDA. GO; GO:0005515; F:protein binding; GO; GO:0006809; P:nitric oxide bios GO; GO:0006810; P:transport; IDA. InterPro; IPR000135; Highmobit_I2. SMR; Q58EV5; 2-84, 93-171. MGI:96113; Hmgbl. NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE MGI; 88

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MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
"Molecular cloning, expression analysis, and chromosomal localization of mouse Hmgl-containing sequences.";
Manm. Genome 5:91-99(1994).
                                                                                                                              1 MGKGDPKKPRGKMSSYAPFVQTCREEHKKKHPDASVNPSEPSKKCSERWKTMSAKEKGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                          Gaps
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P63158; P07155; P27109; P27428;
01-APR-1988 (Rel. 07, Created)
01-ARG-1992 (Rel. 37, Last aquence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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"The mouse gene coding for high mobility group 1 protein (HMG1).";
J. Biol. Chem. 269:28803-28808(1994).
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"Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group protein-1 (HMG1).";
Nucleic Acids Res. 20:3516-3516(1992).
                                                                                      Length 215;
                                                                                                         0; Indels
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                                          PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
SEQUENCE 215 AA; 24894 MW; 8A868DE266D552B5 CRC64;
                                                                                   87.4%; Score 188; DB 2; L
100.0%; Pred. No. 2.2e-160;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Hmgbl; Synonyms=Hmg-1, Hmgl;
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InterPro; IPR000910; HMG 12_box.
Pfam; PR00505; HMG box; 2.
PRINTS; PR00866; HTGHWOBLTY12.
SWART; SM00398; HMG; 2.
                                                                                               al Similarity 100.
188; Conservative
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,
A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J. Usdin T.B., Toohiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00153; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material.
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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SMR; P63158; 1-83, 92-170.

MG1; MG1:96113; Hmgbl.

GO; GO:0005613; C:extracellular space; IDA.

GO; GO:0005634; C:extracellular space; IDA.

GO; GO:0005635; F:nitric-oxide synthase regulator activity; IDA.

GO; GO:0005815; F:procein binding; IPI.

GO; GO:0006810; P:rirric oxide biosynthesis; IDA.

GO; GO:0006810; P:transport; IDA.

InterPro; IPR000135; Highmoblty_12.
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D -> B (in Ref. 3).
B3C6A91FD6F1B133 CRC64;
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HMG box 1.
HMG box 2.
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EMBL, X80457; CAA56611; -; mRNA.
EMBL, L38477; CAA56611.1; -; Genomic_DNA.
EMBL, L38477; AAA57042.1; -; mRNA.
EMBL, BC006586; AAH06586.1; -; mRNA.
EMBL, BC008565; AAH08565.1; -; mRNA.
EMBL, BC008067; AAH83067.1; -; mRNA.
EMBL, BC085090; AAH83067.1; -; mRNA.
PIR, 148688; 148688.
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Pfam; PF00505; HMG_box; 2.
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PRINTS; PR00886; HIGHMOBLTY12.
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2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P63159; P07155; P27109; P27428; 01-ARE-1988 (Rel. 07, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 10-MAY-2005 (Rel. 24, Last sequence update) High mobility group protein 1 (HMG-1) (High mobility group protein 1 (HMG-1) (High mobility Group protein B1) (Amphoterin) (Heparin-binding protein p30).
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MEDLINE-89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
                                         GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                   GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                           DMAKADKARYEREMKTYI PPKGETKKKPKDPNAPKRPPSAFFLFCSEYRPKI KGEHPGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
MEDINES=91389468; PubMed=1885601;
MEDINES=91389468; Debade1885601;
MEDINES=91389468; Debade1885601;
MARTIOVARTA MINIO A SEQUENCE OF SEQUENCE OUTGOOWTH. Amino acid sequence and localization in the filopodia of the advancing plasma membrane.";
J. BIOL. Chem. 266:16722-16729(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal sequence and production of antipeptide antibodies that detect p30 at the surface of neuroblastoma cells and of brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
  Gaps
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MEDLINE=93223672; PubMed=8467791;
Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,
Thomas J.O.;
  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bianchi M.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney, Prostate, and Testis;
NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88067717; PubMed=3684582;
Paonessa G., Frank R., Cortees R.;
"Nucleotide sequence of rat liver HMG1 cDNA.";
"Nucleic Acids Res. 15:9077-9077(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AA
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell Biol. 107:2293-2305(1988)
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                KKKKEEE 188
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=96118376; PubMed=8527432;
Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
Thomas J.O., Laue E.D.;
Thomas J.O., Laue E.D.;
structure of the A-domain of HMG1 and its interaction with DNA as
studied by heteronuclear three- and four-dimensional NNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material.
-!- SIMILARITY: Belongs to the HMG1/HMG2 procein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-structure; Chromosomal protein, Direct protein sequencing, DNA-binding; Heparin-binding; Nuclear protein; Repeat.
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"Structure of the HMG box motif in the B-domain of HMG1."; EMBO J. 12:1311-1319(1993).
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HMG box 2.
Asp/Glu-rich (acidic)
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RGD; 2802; Hmgbl.
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BC081839; AAH81839.1; -; mRNA.
BC088402; AAH88402.1; -; mRNA.
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InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
PRINTS; PR00398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M64986; AAA40729.1; -; mRNA.
EMBL; Y00463; CAA68526.1; -; mRNA.
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PDB; 1AAB; NMR; @=1-83.
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DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120
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                                                                                                           DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
                                                                                                                                                                                                                                                     IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
                                        GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alazawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Schriml L.M., Sakai K., Okido T., Puruno W., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Buromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Aons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N., Satoko K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hansegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body CDNA, RIKEN full-length enriched library, clone:C430013M12 product:high mobility group box 1, full insert sequence. (Fragment).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayaehizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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STRAIN=CS7BL/6J; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBBNMO_MOUSE PRELIMINARY;
Q8BNMO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYRAIN-CSTBL/61; TISSUE=Whole body;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Pukuda S., Puruno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu W., Hirancto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Kawai J., Kojima Y., Konno S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Kurihara C., Saitoh H., Sakai C., Sakazume N., Sano H.,
Sasaki D., Saitoh H., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Angawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yawunishi A., Muramateu M., Hayashizaki Y.,
Tomaru A., Toya T., Yawunishi A., Muramateu M., Hayashizaki Y.,
Bubit AK082902; BAC38678.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Dibbataction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                            ARTAIN=CSTBL/6J; TISSUE-Whole body;
MRDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Nateunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateunuto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Ohara E., Watahiki M., Fujiwake S., Inoue K., Tozawa K., Tanaka T., Natsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
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SMR; QBBNM0; 2-84, 93-171.

MG1; MG1:96113; Hmgbl.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; F:nitric-oxide synthase regulator activity; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

GO; GO:0006810; P:transport; IDA.

InterPro; IPR000115; Highmoblty_12.

InterPro; IPR000115; Highmoblty_12.

InterPro; IPR000110; HMG_12_box.
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100.0%; Pred. No.
STRAIN=C57BL/6J; TISSUE=Whole body;
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PROSITE; PS50118; HMG BOX 2; 2.
NON TER 181
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SM00398; HMG; 2.
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                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simil
Matches 181;
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SEQUENCE
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SEQUENCE
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State Sequence.

MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;

MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;

Maxawa T., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishin Y.,

A Arawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wunshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Landon M. Sandon M., Rawahi M., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUB=Thymus;

MEDLINE=20499374; PubMed=110421159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:C920030B14 product:high mobility group
                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                        full insert sequence. (Fragment).
                                                                                                                          Created)
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STRAIN=C57BL/6J; TISSUE=Thymus;
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                                                                                                      Q8C7C4;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                       QEC7C4 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                   Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
         s 181
                                                                                                                                                                                                                     Name=Hmgb1;
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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tagami M.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                            Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                               Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramcto K., Hiracka T., Hiracan T., Hiramcto K., Hiracka T., Hiramcto K., Hiracana T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Marsuyama T., Miyazaki A., Murata M., Nakamura M., Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tomaru A., Takahashi F., Takaku-Akahira S., Takada T., Tanaki T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:000515; F:nitric-oxide synthase regulator activity; IDA.
GO; GO:0005515; F:nitric oxide biosynthesis; IDA.
GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
GO; GO:0006810; P:transport; IDA.
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Last annotation update)
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100.0%; Pred. No. 1.7e-151;
iive 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK050659; BAC34367.1; -; mRNA.
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InterPro; IPR000910; HMG 12 box.
Pfam; PF00505; HMG box; 2.
                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Thymus;
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Q9QX40;
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                                                                                                                                                                                                                                                                                                                              SEQUENCE
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les 178; Conserv
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56 EKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDDNAPKRPPSAFFLFCSEYRPKIKG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 EHPGLSIGDVAKKUGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGV 175
                                                                                                                     Lee K.-1.D., Lum H.-K., Nevo E.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078820; AAC27653.2; -; Genomic_DNA.
R HSBP; P07156; 1NHN.
R SMR; Og0X40; 2-84, 93-171.
R GO; GO:0000785; C:chromatin; IEA.
R GO; GO:00005634; C:nucleus; IEA.
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0005635; P:Cequlation of transcription, DNA-dependent; IEA.
R GO; GO:000135; Highmoblty_12.
R InterPro; IPR000135; Highmoblty_12.
R InterPro; IPR00010; HMG 12_box.
R Pfam; PR00565; HMG Dox; Z.
R PRINTS; RR00886; HIGHMOBLTY12.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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EMBL; AL153648; CAI15604.1; -; Genomic_DNA.

EMBL; AL153648; CAI15604.1; -; Genomic_DNA.

GO; GO:0000785; C:chromatin; IEA.

GO; GO:0000534; C:nucleus; IEA.

GO; GO:0000535; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000135; Highmoblty_12.

R Pfam; PF00055; HMG box; Z.

R Pfam; SM00386; HMG box; Z.

R PROSITE; PS00135; HMG BOX 1; 1.

R PROSITE; PS00135; HMG BOX 1; 1.

R PROSITE; PS50118; HMG; Z.

R PROSITE; PS50118; HMG; Z.
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Pred. No. 3e-135;
0; Mismatches 0; Indels
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PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24895 MW; 599FBBA6FDF41F17 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment)
Name-iMGE1; ORFNames-RP11-550P23.1-009;
Homo sapiens (Human)
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100.0%; Pred. No. ...
0; Mismatches
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Muridae; Spalacinae; Nannospalax
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QST7C2;
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        Query Match
        73.0%;
        Score 157;
        DB 2;
        Length 157;

        Best Local Similarity 100.0%;
        Pred. No. 1.10-132;
        0;
        Gaps 0;

        Matches 157;
        Conservative 0;
        Mismatches 0;
        Indels 0;
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        0
        0

        Db
        1 MGKGDPKKPRGKMSYAFFVQTCREEHKKKFKDPAASVNFSEFSKKCSERWKTMSAKEKGKF 60
        0

        Qy
        61 EDWAKADKARYEREMKTY1PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

        Db
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        Qy
        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKIKEKYEK 157

        Db
        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKIKEKYEK 157
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Search completed: April 6, 2006, 10:40:42 Job time : 231 secs

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US-09-214-881A-1
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Sequence 4, Appli
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Sequence 10813, A
Sequence 4826, Ap
Sequence 1018, Ap
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Sequence 1, Appli
Sequence 10728, Ap
Sequence 10728, Ap
Sequence 11, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 11, Appli
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Sequence 1, Appli
                                                                    April 6, 2006, 10:40:58; Search time 46 Seconds (without alignments) 386.419 Million cell updates/sec
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215
1 MGKGDPKKPRGKMSSYAFFV......DEEEBEDEEDEBDEDDDB
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-214-881A-1
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US-09-214-881A-5
US-09-513-999C-7904
US-09-513-999C-4824
US-09-513-999C-4824
US-09-513-999C-4826
US-09-513-999C-4826
US-09-513-999C-4826
US-09-513-999C-4826
US-09-514-981A-2
US-09-214-881A-8
US-09-214-881A-8
US-09-214-881A-11
US-09-214-881A-11
US-09-214-881A-13
US-08-16-558-8
US-08-16-558-8
US-08-16-558-8
US-08-249-322A-8
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                                                OM protein - protein search, using sw model
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No.
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Sequence 8, Appli Sequence 9, Appli Sequence 12, Appl Sequence 12, Appl Sequence 324, Appl Sequence 324, Appl Sequence 324, Appl Sequence 789, Appl		Method of Using Same	1429	Length 214; ; Indels 0; Gaps 0;	KKCSERWKTMSAKEKGKFE 61 	PELFCSEYRPKIKGEHPGLS 121	RAKGKPDAAKKGVVKAEKS 181 RAKGKPDAAKKGVVKAEKS 180
US-08-469-526A-8 US-08-734-591A-8 US-08-469-660-8 US-08-469-660-8 US-08-735-021-8 US-08-735-021-8 US-08-734-664A-8 US-08-734-664A-8 US-08-734-664A-8 US-08-735-021-8 PCT-US94-05093C-8 PCT-US95-06846A-8 US-09-214-881A-24 US-09-702-705-705-789 US-09-702-705-789 US-09-736-457-789 US-09-736-457-789 US-09-736-457-789 US-09-736-457-789	ALIGNMENTS	omplexes and, 092	ACCENTION: (1)(0)(Score 214; DB 2; Pred. No. 2.6e-187); Mismatches 0;	GKGDPKKPRGKMSSVAFFVOTCREEHKKKHPDASVNFSBFSKKCSBRWKTMSAKEKGKFB 	DVAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPCLS 	IGDVAKKLGEMMINITAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS
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		ULT 1 Gquence 883, Application US/ Vatent No. 6753314 GREAL INFORMATION: GAPLICANT: Giot, Loic APPLICANT: Mansfield, Traci TITLE OF INVENTION: Protein- FILE REFERENCE: 15966-542 CURRENT FILING DATE: 2000-0 PRIOR APPLICATION NUMBER: 6 PRIOR APPLICATION NUMBER: 60 PRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 2000-02-0 RIOR FILING DATE: 2000-02-0 RIOR FILING DATE: 2000-02-0 RIOR PILING DATE: 2000-02-0 RIOR FILING DATE: 2000-02-0 RIOWER OF SEC ID NOS: 1387 SOFTWARE: CURPATSESGFORMATE ELENGTH: 214 TYPE: PRT CREANIES: HRT ORGANISM: HOMO SADIENS FEATURE: PRT	(0)(0) RMATION: 1 883	99. Similarity 100 4; Conservative	GKGDPKKPRGKMSSYAF 	MAKADKAR MAKADKAR	GDVAKKLGI GDVAKKLGI
		RESULT 1 US-09-538-092-883 Sequence 883, Applic Patent No. 6753314 GENERAL INFORMATION: APPLICANT: Giot, Lo. APPLICANT: Manefie; TITLE OF INVENTION: FILE REFERENCE: 159 CURRENT APPLICATION NO. CURRENT FILING DATE: PRIOR APPLICATION NO. SOFTWARE: CLIARG DATE: PRIOR PILING DATE: PRIOR FILING DATE: PRIOR APPLICATION NO. SOFTWARE: CLIARDELSE DEN ORGANISM: HOMO 883 LENGTH: 214 TYPE: PRT ORGANISM: HOMO 889 LENGTH: 214 TYPE: PRT ORGANISM: HOMO 899	LOCATION: (0 OTHER INFORM 9-538-092-88	Query Match Best Local Si Matches 214;	1 6 0 – 0	62 D 61 D	122 I
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Matches 205; Conservative
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                                                                                          APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usaaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TILE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06833.0.104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Sobajima, Junko
APPLICANT: Useudi, Hiroko
APPLICANT: Useudi, Hiroko
APPLICANT: Useudi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funio
APPLICANT: Osakada, Funio
APPLICANT: Osakada, Funio
APPLICANT: Userbernor: Useudia APPLICANT: Useudi
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Sequence 1, Application US/09214881A
Patent No. 6822078
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Patent No. 6822078
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ORGANISM: Homo sapiens
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Best Local Similarity
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; ORGANISM: Bos taurus
US-09-214-881A-3
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LENGTH: 214
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Best Local Similarity

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61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120
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0; Gaps
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### APPLICANT Sobajim Junko
### APPLICANT Ucasuji, Hiroko
### APPLICANT Tanaki, Masao
### APPLICANT Tanaki, Masao
### APPLICANT Shirakawa, Hitoshi
### APPLICANT Yoshida, Michiteru
### APPLICANT Shirakawa, Hitoshi
### APPLICANT Osakada, Fumio
### TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
### PER REFERENCE: 068983.0104
### CURRENT PILLING DATE: 1999-06-07
### SOFTWARE PATENTIN NUMBER: US/09/214,881A
### SOFTWARE PATENTIN VON. 2.1
### SEQ ID NOS: 13
### SEQ ID NOS: 13
### SEQ ID NOS: 13
### SEQ ID NOS: 14
### SEQ ID NOS: 17
### TYPE: PF***
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0; Mismatches
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US-09-214-881A-5
US-09-214-881A-5
Sequence 5, Application US/09214881A
Patent No. 6822078
GENERAL INFORMATION
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Sobajima, Junko
Uesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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ORGANISM: Human
US-09-949-016-10813
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Patent No. 6783961

GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOSTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Sakada, Funio
ITILE OP INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILLE REFERENCE: 668383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1399-06-07
SOFTWARE: Paterite: 1399-06-07
SSOFTWARE: Paterite: 13
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                                                                                                                                                                                                                                                                                                                                                Query Match 65.1%; Score 140; DB 2; Length 214; Best Local Similarity 100.0%; Pred. No. 7.1e-120; Matches 140; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.6%; Score 98; DB 2; Length 101; 100.0%; Pred. No. 7.2e-82;
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                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-513-999C-7904
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US-09-949-016-10813
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US-09-513-999C-7904
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                                                                                                                                                                                                                                   SEQ ID NO 5
LENGTH: 214
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TYPE: PRT
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERRACE: CLOOL307;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10013

LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 YRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 YRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REFERENCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PETENT. PM
SOFTWARE: PETENT. PM
SEQ ID NO 4824
LENGTH: 110
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Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92; DB 2; Le
Pred. No. 3.9e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 DAAKKGVVKAEKSKKKKEEEDEEDEEDEEEE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.8%; bcc. 100.0%; Pred. No. ... 0; Mismatches
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CACATION: 91
CHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Marches 92; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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STREET: 12.
TTV: Boston
US-09-513-999C-4826
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; Sequence 4826, Application US/09513999C
; Batent No. 678361
; GENERAL INFORMATION:
; APPLICANT: Dumas Milh. Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Diclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PALCH No. 678361
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT APPLICATION NUMBER: US 60/122,487
; PRIOR PLING DATE: 1999-02-26
; VANBER OF SEQ ID NOS: 36681
; SOFTWARE: PALCHL.PM
; SEQ ID NO 4826
; LENGTH: 59
; TYPE: PRT

ORGANISM: Homo sapiens
                               Sequence 4825, Application US/09513999C
Sequence 4825, Application US/09513999C
Fatent No. 678361
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFRERENCE: 59.192.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOUTHWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 KHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKF 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 12
OTHER INFORMATION: Xaa=Glu or Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: UNSURE
LOCATION: 17
OTHER INFORMATION: Xaa=Ala or Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 91
COTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4825
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: UNSURE
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NAME/KEY: UNSURE
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               US-09-513-999C-4825
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LENGTH: 110
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; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Glot, Loic
; TITLE OF INVENTION Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
                                                      Gaps
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APPLICANT: TAKADA, Yukihiro
APPLICANT: YAMAMURA, Junichi
APPLICANT: GOTO, Masaaki
APPLICANT: GOTO, Masaaki
APPLICANT: AOE, Selichiro
TITLE OF INVENTION: An Agent Promoting Bone Formation and
TITLE OF INVENTION: Inhibiting Bone Resorption
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: 125 High St.
Query Match 18.1%; Score 39; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 2.7e-28; Matches 39; Conservative 0; Mismatches 0; Indels
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ZIP: 0210
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CUMBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,545
FILING DATE: 20-FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, Paula A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: PJN-054
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: CLASSIFICS:
                                                                                                     52 MSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFK 90
                                                                                                                                                    1 MSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFK 39
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                                                                                                                                                                                                                                                                    Sequence 1, Application US/08803545
Patent No. 5851986
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 30; Conservative
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LENGTH: 30 amino acids
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APPLICANT: Sobajima, Junko
APPLICANT: Usuguj, Hiroko.
APPLICANT: Usuguj, Hiroko.
APPLICANT: Usuguj, Hiroko.
APPLICANT: Tanaka, Masao.
APPLICANT: Nakao, Kazwa
APPLICANT: Nakao, Kazwa
APPLICANT: Shirkawa, Hitoshi
APPLICANT: Shirkawa, Hitoshi
APPLICANT: Shirkawa, Hitoshi
APPLICANT: Olaskada, Fumio
APPLICANT: Olaskada, Fumio
APPLICANT: Olaskada, Fumio
APPLICANT: Shirkawa, Hitoshi
APPLICANT: Olaskada, Fumio
APPLICANT: Shirkawa, Hitoshi
APPLICANT: Joshi
APP
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
CURRENT APPLICATION NUMBER: US/09/538,092;
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPACSEQFORMATLET VERSION 0.9
SOFTWARE: CURAPACSEQFORMATLET VERSION 0.9
LENGTH: 208
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Sobajima, Junko
Uesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-09-214-881A-2
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APPLICANT: Ozaki, S
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US-09-214-881A-6
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APPLICANT: Ozaki, Shoichi
APPLICANT: Ozaki, Junko
APPLICANT: Obasim, Junko
APPLICANT: Tanaka, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: 1999-06-07
NUMBER OF SEQ IN OSS: 13
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           APPLICANT: Shirakawa, Hitchia
APPLICANT: Shirakawa, Hitchia
APPLICANT: Shirakawa, Hitchia
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 066983.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Var. 2.1
SEQ ID NO 6
LENGTH: 209
TYPE: PRT
ORGANISM: Sus scrofa
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Pred. No. 5.3e-16;
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100.0%; Pred. No. ...
0; Mismatches
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Yoshida, Michiteru
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Matches 26; Conservative
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Sequence 37, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 17, Appl
Sequence 177, Appl
Sequence 175, Appl
Sequence 1055, Ap
Sequence 1055, Ap
Sequence 18, Appl
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Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
ITILE OF INVENTION: ONCEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOWEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ONCEL COMPOSITIONS AND METHODS FOR CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2000-13-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 215
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                        US-10-938-992-37
US-09-214-881A-4
US-09-214-881A-5
US-10-726-195-4
US-11-0726-195-4
US-11-013-684-17
US-09-925-300-1757
US-09-925-299-1055
US-10-106-698-6757
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llarity 100.0%; Pred. No. 6e-173;
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2: /cgn2 6/ptodata/1/pubpaa/USG08 PUBCOMB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-71-948-55-1
US-10-868-577A-63
US-10-868-577A-63
US-10-868-577A-63
US-10-98-592-74
US-10-98-592-74
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US-10-938-992-36
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TYPE: PRT
ORGANISM: Homo Sapien
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Sequence 1, Application US/10300072

Publication No. US20030144201A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Howland Shaw Warren, Jr.

APPLICANT: Mitchell P. Fink

ITILE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY

ITILE OF INVENTION: AGENTS

FILE REFERENCE: 3268.1001-005

CURRENT APPLICATION NUMBER: US/10/300,072

CURRENT FILING DATE: 2002-11-20

FRIOR PELING DATE: 2002-05-15

PRIOR PELING DATE: 2002-05-15

PRIOR APPLICATION NUMBER: US 60/291,034

PRIOR PILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PERSENCE: 58

SOFTWARE: PERSENCE: 38

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SEQ ID NOS: 58

SEQ ID NOS: 58
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100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6e-173;
tive 0; Mismatches 0;
       APPLICANT: ABOUT APPLICANT: APPLICANT: Warren Jr., Howland Shaw APPLICANT: Warren Jr., Howland Shaw APPLICANT: Warren Jr., Howland Shaw APPLICANT: Fink, Mitchell P. ITILE OF INVENTION: Use of HMG Fragments as TITLE OF INVENTION: 3268.1001-001
FILE REFERENCE: 3268.1001-001
FURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 215
APPLICANT: Tracey, Kevin J.
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Best Local Similarity 100.
Matches 215; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Kevin J. Tracey

TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

FILE REFERENCE: 3268.1001-007

CURRENT APPLICATION NUMBER: US/10/456,947

PRIOR APPLICATION NUMBER: 10/147,447
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100.0%; Score 215; DB 4;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0;
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APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
FILE REFERENCE: 3268.1001-006
CURRENT APPLICATION NUMBER: US/10/456,949
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FARESEQ for Windows Version 4.0
LENGTH: 215
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Publication No. US20040005316A1
GENERAL INFORMATION:
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Publication No. US20050032697A1

GENERAL INFORMATION:
APPLICANT: Alitalo et al.
TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
FILE REFERENCE: 28967/33359A

CURRENT APPLICATION NUMBER: US/10/868,577A

CURRENT FILING DATE: 2004-06-14

PRIOR APPLICATION NUMBER: US 60/478,390

PRIOR APPLICATION NUMBER: US 60/478,390

PRIOR APPLICATION NUMBER: US 10/669,176

PRIOR APPLICATION NUMBER: US 10/669,176

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Patentin version 3.2

LENGTH: 215
                                 US-10-17,
Sequence 1, Application US/10717984
Sequence 1, Application US/10717984
Publication No. US20040156851A1
GENERAL INFORMATION:
APPLICATION Newman, Walter
TITLE OF INVENTION: HMGBI COMBINATION THERAPIES
FILE REFERENCE: 3258.1008-001
CURRENT FILING DATE: 2003-11-20
FRIOR PILING DATE: 2003-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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100.0%; Score 215; DB 4;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0;
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; Pred. No. 6e-173;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 215; Conservative 0
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ORGANISM: Homo sapiens
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Publication No. US20040141948A1

GENERAL INFORMATION:
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
CURRENT FILING DATE: 2003-11-12
PRIOR PILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 215
                                                                                                                                                                                                                                                                                                                        Matches 215; Conservative
                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                   Sequence 22, Application US/10868549
Publication No. US20050043235A1
GENERAL INFORMATION:
TITLE INFORMATION: USE OF USEF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
FILE REFERENCE: 28967/39117A
CURRENT APPLICATION NUMBER: US 60/478,114
PRIOR APPLICATION NUMBER: US 60/478,114
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
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APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
APPLICANT: Obsr. Robert
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REFERENCE: 3258.1033-001
CURRENT FILING DATE: 2004-09-10
FRIOR APPLICATION NUMBER: 60/502,568
PRIOR FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SEQ ID NO 74
SEQ ID NO 74
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GENERAL INFORMATION: APPLICANT: Newman, Walter
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ORGANISM: Homo sapiens
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LENGTH: 215
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APPLICANT: OZaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Macao
APPLICANT: Tanaka, Macao
APPLICANT: Nakao, Karwa, Hitoshi
APPLICANT: Shidaka, Michiteru
APPLICANT: Shizakawa, Hitoshi
APPLICANT: Shizakawa, Hitoshi
APPLICANT: Shizakawa, Hitoshi
APPLICANT: Osakada, Funio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: 06838.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 214
TYPE: PPP
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                                                                                                        Query Match 100.0%; Score 215; DB 5; Length 215; Best Local Similarity 100.0%; Pred. No. 6e-173; Matches 215; Conservative 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-74
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Query Match
Best Local Similarity 100.0
Matches 214; Conservative
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US-10-938-992-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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                                                                                                         APPLICANT: Osbailon:
APPLICANT: Sobailma, Junko
APPLICANT: Sobailma, Junko
APPLICANT: Usesaki, Hiroko
APPLICANT: Usesaki, Hiroko
APPLICANT: Usesaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Punia
APPLICANT: Osakada, Punia
APPLICANT: Wondawa, Hitoshi
APPLICANT: Osakada, Punia
APPLICANT: Shirakawa, Hitoshi
APPLICANTON: Shirakawa, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%; Score 214; DB 5; Length 214; 100.0%; Pred. No. 4.2e-172; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 KKKKEEEEDEEDEEDEEDEEDEEDEEDEEDDDDE 215
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                      ; Sequence 1, Application US/10726195; Publication No. US20040229279A1; GENERAL INFORMATION:
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US-10-938-992-40
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ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-10-938-992-40
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LENGTH: 214
   US-10-726-195-1
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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 IGDVAKKIGEMMINITAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 187
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99.5%; Score 214; DB 5; Length 221; 100.0%; Pred. No. 4.3e-172; ive 0; Mismatches 0; Indels
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| Sequence 38, Application US/10938992|
| Publication No. US20050152903A1|
| Publication No. US20050152903A1|
| GENERAL INFORMATION:
| APPLICANT: Oin, Shaxin
| APPLICANT: O'Keefe, Therea APPLICANT: O'Keefe, Therea APPLICANT: O'Keefe, Therea APPLICANT: O'Keefe, Thoreac APPLICANT: APPLICANT: O'Keefe, Thoreac APPLICANT: APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
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61 DWAKADKARYEREMKTYIPPKGETKKKKFKDPNAPKRPDSAFFLFCSEYRPKIKGEHPGLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Karuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 069383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.3%; Score 205; DB 3; Length 214; Best Local Similarity 100.0%; Pred. No. 1.6e-164; Matches 205; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Bos taurus
US-09-214-881A-3
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Search completed: April 6, 2006, 10:45:14 Job time : 168 secs

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US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1
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12, App 1
13, App 1
13, App 1
134, App 1
1, App 1
2, App 1
2, App 1
12397, A
6675, A
12021, A
142, App 1
12397, A
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9681, Ap
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3511, Ap
13611, A
26884, A
                                                                                                                                                               6, 2006, 10:42:38; Search time 24 Seconds (without alignments) 279.428 Million cell updates/sec
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Sequence 6
Sequence 3
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Sequence 1
Sequence 5
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1 MGKGDPKKPRGKWSSYAFFV.....DEEEEEDEEDEEDEDDDB
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2: /SIDSS/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
3: /SIDSS/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
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GenCore version 5.1.7
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US-11-186-422-12

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US-11-166-422-13

US-11-166-421-133

US-11-166-04-1234

US-11-196-04-1234

US-10-19-150-1

US-10-19-150-1

US-11-044-899-30

US-11-044-899-30

US-11-047-899-30

US-11-047-899-30

US-11-047-899-30

US-11-047-899-30

US-11-096-568A-6675

US-11-096-568A-6675

US-11-096-568A-9681

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                                                                                                             - protein search, using sw model
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length: 2000000000
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Maximum DB e
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No.
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Sequence 1443, Application US/10821234

Sequence 1443, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

FRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER: OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ_Genes Version 1.0

SEQ ID NO 1443

LENGTH: 215
Sequence 1564, Ap Sequence 31073, Ap Sequence 4976, Ap Sequence 1554, Ap Sequence 1554, Ap Sequence 1571, Ap Sequence 1566, Ap Sequence 1566, Ap Sequence 1566, Ap Sequence 2474, Ap Sequence 2680, App 
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                                                US-11-087-099-9185
US-11-087-099-4976
US-11-082-234-1569
US-11-087-099-3510
US-11-087-099-3510
US-11-087-099-3510
US-11-087-099-3510
US-11-087-099-9017
US-11-096-568A-9680
US-11-096-568A-9680
US-11-096-568A-9810
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Best Local Similarity 100.
Matches 215; Conservative
     , ORGANISM: Homo sapiens
US-10-821-234-1443
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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                          121 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEKKAAKLK 152
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Sequence 6, Application US/10719150

Sequence 6, Application No. US20040120953A1

SEDERAL INFORMATION:
APPLICANT: Haichao Wang
TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING
TITLE OF INVENTION: ANTAGONISTS OF MGI FOR TREATING
TITLE OF INVENTION: ANTAGONIST OF HMGI FOR TREATING
FILE REFERENCE: 3269.100-0.11

CURRENT FILING DATE: 2003-11-21

PRIOR PLING DATE: 2002-11-20

PRIOR FILING DATE: 2002-07-31

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 1999-02-11

SPRIOR FILING DATE: 1999-02-11

SPRIOR FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 6

SOFTWARE FARENCE FARENCE FALENCE OF WINDOWS VERSION 4.0

SEQ ID NO 6

LENGTH: 54

TYPE: PRT

TYPE: PRT

CREANISM: Homo Sapiens
                                                                                                                                                                                                                                                                     153 EKYEKDIAA 161
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ORGANISM: Homo sapiens
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87.4%; Score 188; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-167;
Matches 188; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 215; DB 7; Length 2: Best Local Similarity 100.0%; Pred. No. 1.3e-192; Matches 215; Conservative 0; Mismatches 0; Indels
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APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Refe, Thereaa
APPLICANT: Luciano, Peter
APPLICANT: Qin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT APPLICATION NUMBER: 00/589,678
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR PILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-11-186-422-12
i Sequence 12, Application US/11186422
i Publication No. US2006005/679A1
i GENERAL INFORMATION:
i APPLICANT: Critical Theresa
i APPLICANT: Critical Theresa
i APPLICANT: Luciano, Peter
i APPLICANT: Luciano, Peter
i APPLICANT: Q. Shixin
i TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
i FILE REFERENCE: 3258.1021-003
i CURRENT FILINO DATE: 2005-07-20
i PRIOR APPLICATION NUMBER: 05/589,678
i PRIOR FILING DATE: 2004-07-20
i NUMBER OF SEQ ID NOS: 34
i SOFTWARE: FastSEQ for Windows Version 4.0
i SEQ ID NO 12
i LENGTH: 215
i TYPE: RRT
i ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-11
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US-10-719-150-6

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                                                     Sequence 1224, Application US/10821234

Sequence 1224, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat. Ivan

APPLICANT: Adarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT FILING DATE: 2004-04-07

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt SeQ genes Version 1.0

SEQ ID NO 1234
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Sequence 1, Application No. US20040120953A1

GENERAL INFORMATION:
APPLICANT: Revin J. Tracey
TITLE OF INVENTION: ANTAGONISTS OF HMG1 FOR TREATING
TITLE OF INVENTION: INFLAMMATORY CONDITIONS
FILE REFERENCE: 3268.1000-011
CURRENT APPLICATION NUMBER: US/10/719,150
CURRENT FILING DATE: 2003-11-21
PRIOR FILING DATE: 2002-11-20
PRIOR PRILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 10/210,747
PRIOR APPLICATION NUMBER: US 09/503,632
PRIOR FILING DATE: 2000-02-07-31
PRIOR FILING DATE: 2000-02-07-31
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing (S-10-821-234-1234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.3%; Score 20; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 14; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-719-150-1
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TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REPERBACE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT APPLICATION NUMBER: 60/584,405
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR PILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                            32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET
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Query Match 25.1%; Score 54; DB 6; Length 54; Best Local Similarity 100.0%; Pred. No. 2e-43; Matches 54; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Ordefe, Theresa
APPLICANT: Ordefe, Theresa
APPLICANT: Ordefe, Theresa
APPLICANT: Qin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT FILING DATE: 2005-07-20
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR SEQ ID NOS: 34
SOFTWARE PARTESEQ for Windows Version 4.0
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/11186422
Publication No. US20060057679A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 54; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 22; Conserva
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LENGTH: 879
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JUNEARL INFORMATION:

APPLICANT: Schwab, M.
APPLICANT: Chem, M.
TITLE OF INVENTION: WUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
TITLE OF INVENTION: THEREON
FILE REFERENCE: 10200-017-999
CURRENT APPLICATION NUMBER: 02/11/044,899
CURRENT FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: 09/830,972
PRIOR APPLICATION NUMBER: PT/US99/26160
PRIOR APPLICATION NUMBER: PT/US99/26160
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 1163
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
TITLE REPERENCE: 30-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 1750
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Pred. No. 0.00061;
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; Sequence 28367, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
                                                                                                                                      US-11-044-899-30
Sequence 30, Application US/11044899
Publication No. US20050260616A1
GENERAL INFORMATION:
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US-11-087-099-12397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 DEEEEEDEEDE 208
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33 EDEEDEEEEDEE 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-087-099-12397
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## Sequence 2, Application US/11044899
## Publication No. US20050260616A1
## CAPLICANT: Schwab, M.
## APPLICANT: Schwab, M.
## APPLICANT: Schwab, M.
## TITLE OF INVENTION: THEREON
## TITLE OF INVENTION: THEREON
## TITLE OF INVENTION: THEREON
## FILE REFERENCE: 10200-017-999
## CURRENT APPLICATION NUMBER: US/11/044,899
## CURRENT APPLICATION NUMBER: US/830,972
## PRIOR PPLICATION NUMBER: PCT/US99/26160
## PRIOR PPLICATION NUMBER: PCT/US99/26160
## PRIOR PPLICATION NUMBER: PCT/US99/26160
## PRIOR PPLICATION NUMBER: 60/107,446
## PRIOR PPLICATION NUMBER: 60/107,446
## PRIOR PPLICATION NUMBER: 60/107,446
## PRIOR PPLICATION NUMBER: 50/107,446
## PRIOR PPLICATION NUMBER: 50/107
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                                                                                                                   Sequence 4, Application US/10719150
| Sequence 4, Application No. US20040120953A1
| GENERAL INFORMATION:
| APPLICANT: Kevin J. Tracey
| APPLICANT: Haichao Wang
| TITLE OF INVENTION: INFLAMMATORY CONDITIONS
| TITLE OF INVENTION: INFLAMMATORY CONDITIONS
| FILE REFERENCE: 3268.1000-011
| CURRENT APPLICATION NUMBER: US/10/719,150
| CURRENT FILING DATE: 2003-11-21
| PRIOR APPLICATION NUMBER: US/10/300,068
| PRIOR APPLICATION NUMBER: US/10/300,068
| PRIOR FILING DATE: 2002-01-31
| PRIOR APPLICATION NUMBER: US/10/300,747
| PRIOR FILING DATE: 2002-07-31
| PRIOR FILING DATE: 2002-07-31
| PRIOR FILING DATE: 1999-02-11
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ORGANISM: Artificial Sequence
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; ORGANISM: Rattus sp.
US-11-044-899-2
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592P025
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 28367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6675, Application US/11096568A
Sequence 6675, Application No. US20060048240A1
Sequence 6675, Application No. US20060048240A1
GENERAL INFORMATION:
TIPLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 210-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
SEQ ID NOS: 34471
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NAMENKEY: misc feature
LOCATION: (1).7(106)
LOTTER INFORMATION: Ceres Seq. ID no. 14316260
US-11-096-568A-6675
                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

LOCATION: (1)..(447)

CTHER INFORMATION: Ceres Seq. ID no. 2715782

US-11-096-568A-28367
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Job time : 24 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AAE35863	AD025922	AD071481	AD025934	AD071527	ADY85362	ADY85078	ADY85087	ADR45941	AD025962	AD071534	ADY85368	ADY85084	AAB57179	ABM81641	ADA55380	ADD47645	ADE60730	ADE60447	ADE57980	ADE57984	ADE57978	ADE60732	ADE57982
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ALIGNMENTS

Rat; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis, hepatitis; appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis; allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease; amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene therapy; human immunodeficiency virus; mouse; human; HMGBI protein. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. (GEHO) GEN HOSPITAL CORP. (UYPI-) UNIV PITISBURGH. MΡ; Fink 69 AA Tracey KJ, Yang H, Warren HS, 15-MAY-2002; 2002WO-US015329. 15-MAY-2001; 2001US-0291034P AAE35863 standard; protein; entry) (first WO200292004-A2. Mus sp. Rattus sp. Homo sapiens. 21-NOV-2002. 17-JUN-2003 HMG1 B box AAE35863; RESULT 1 AAE35863

WPI; 2003-120594/11.

New isolated polypeptide having a vertebrate HWG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.

Disclosure; Fig 12E; 82pp; English.

immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human/mouse/rat high mobility group box 1 (HMG1) B box protein sequence that can be used to stimulate cytokine activity and increase immune response to assist in

comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of

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Gaps

; 0

Length 69; Indels

; Score 370; DB 8; ; Pred. No. 3.7e-38; 0; Mismatches 0;

100.08; 100.08;

Query Match
Best Local Similarity 100.
Matches 69; Conservative

treating disease

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Sequence 69 AA;

9 9

1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK

EKYEKDIAA 69

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EKYEKDIAA 69

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The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-actuaring HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by convention of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, asthma, allergy, immune complex disease, sinusitis, amochiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, and an inflammatory atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is HMGI (also termed as HMGBI) B box found in human, mouse and rat
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                                                                                                                                                                                                                                                                                                100.0%; Score 370; DB 6; Length 69; 100.0%; Pred. No. 3.7e-38;
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Human/mouse/rat high mobility group box 1 (HMGB1) B box protein.

(first entry)

26-AUG-2004

ADO71481;

ADO71481 standard; protein; 69 AA

RESULT 3

ADO71481

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Human; mouse; high mobility group box 1 B box; HMGB1 B box; HMGB, thMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; repartionis, myocardial ischaemia; organic ischaemia; repartusion ischaemia; Behcet's disease; graft-versus-host disease; crohn's disease; ulcerative colitis; multiple sclerosis; cachexia; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a polypeptide comprising a high mobility group box protein (HWGB) A or B box, The HWGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 32; SEQ ID NO 5; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2002; 2002US-0427841P.
20-NOV-2002; 2002US-0427846P.
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                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                               Rattus sp.
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New pharmaceutical composition comprises a polypeptide comprising an HMGB B box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.

WPI; 2004-420625/39.

Disclosure, SEQ ID NO 5; 68pp; English.

The invention describes a pharmaceutical composition comprising a polypeptide comprising an HWGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide

us-10-717-984-5.rag

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specifically bind to the HWGB B box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinflammentory cytokine from a cell treated with HMGB, a method for effecting weight loops or treating obseity in a patient, a method of determining whether a compound inhibite inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obseity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obseity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepais, allograft rejection, rheumatoid arthritis, asthma, luques, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritornitis, untiple sclerosis or cachexia. This sequence contents a human/mouse/rat HMGBI B box polypeptide of the invention.
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HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEKKAAKLK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 370; DB 8; Length 69; 100.0%; Pred. No. 3.7e-38; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO25934 standard; peptide; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-2003; 2003WO-US036975.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.
69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKYEKDIAA
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 69 AA;
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinfiammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to one-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immune response in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) B box biologically active fragment.
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                                                                                                                                                                                                                                                                                                                                                                           5 NAPKRPPSAFFLFCSEXRPKIKGEHPGLSIGDVAKKLGEMWINTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                      1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatoid arthritis; asthma; lupus; adult respiratory distress syndchronic obstructive pulmonary disease; psoriasis; pancreatitis; perilonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; crohn's disease; crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
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                                                                                                                                                                                                                                                                       DB 8; Length 74;
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human high mobility group box (HMGB) B box protein #1.
                                                                                                                                                                                                                                                                     100.0%; Score 370; DB 8; 100.0%; Pred. No. 4e-38; iive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 51; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO71527 standard; protein; 74 AA.
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20-NOV-2002; 2002US-0427846P.
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                                                                                                                                                                                                                                                                                                              69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     EKYEKDIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004046345-A2
                                                                                                                                                                                                                                 Sequence 74 AA;
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Disclosure; SEQ ID NO 37; 57pp; English.

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composition weight loss or treating obesity in a patient, a method for effecting weight loss or treating obesity in a patient, a method of detecting weight loss or treating obesity in a patient, a method of ceternianing whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TNF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, chronic obstructive pulmonary disease, psoriasis, pancreatitis, chronic obstructive pulmonary disease, psoriasis, pancreatitis, chronic batchevis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, behcet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB B box polypeptide of the invention.
   epitopes of HMGB, where the antibodies can inhibit release of a
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Sequence 74 AA;

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64
                                                                                       NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLK
                                                                     1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                       0; Gaps
100.0%; Score 370; DB 8; Length 74; 100.0%; Pred. No. 4e-38; ive 0; Mismatches 0; Indels
                 l Similarity 100.0%;
69; Conservative 0
                                                                                                                                        61 EKYEKDIAA 69
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 Query Match
Best Local Similarity
                                     Matches
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ADY85362 standard; protein; 74 AA. ADY85362;

(first entry) 02-JUN-2005

Human high mobility group box protein HMGB1 B box.

immunosuppressive; autoimmune disease; allergy; antiallergic; ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiasthmatic; rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer High mobility group box; HMGB1; immune disorder; infection;

Homo sapiens

WO2005025604-A2.

24-MAR-2005.

.0-SEP-2004; 2004WO-US029540.

(GEHO) GEN HOSPITAL CORP. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. 10-SEP-2003; 2003US-0502349P.

Warren HS, Tracey KJ;

WPI; 2005-233421/24.

Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment.

The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural HMGB A box. The immune cell fragment of the vertebrate or non-natural HMGB A box. The immune antigen, non-self material (e.g. a cell or tissue such as bone marrow cells) or adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of adjuvant to the individual, by the transplantation of an organ into the individual or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune response to an administered non-human antigen comprise administering a HMGB A box, a non-naturally-occurring HMGB A box, a non-naturally-occurring HMGB A box, a claimed method of treating an autoimmune disorder in an individual comprises administering a HMGB polypeptide comprising a vertebrate and a vertebrate or non-naturally-occurring HMGB box. The HMGB polypeptide is preferably a HMGBI peptide and may be fragment of these, and a vertebrate or non-naturally-occurring HMGB box. The HMGB polypeptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is alleray, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, securing the B box of human HMGBI protein ADY85326. ö 9 64 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK Gaps ; 0 9; Length 74; ; Score 370; DB 9; Length 7; Pred. No. 4e-38; 0; Mismatches 0; Indels Query Match

Best Local Similarity 100.0%;

Matches 69; Conservative 0; Sequence 74 AA; ò

S NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 61 EKYEKDIAA 69 EKYEKDIAA 73 셤 d ò

RESULT 7 ADY85078

ADY85078 standard; protein; 74 AA. ADY85078;

16-JUN-2005 (first entry)

Human HMGB1 A box.

sepsis, antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiasthmatic; lupus erythematosus; antianthmaticy; lupus erythematosus; antianthmaticy; lupus erythematosus; respiratory distress syndroms; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behocts disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen.; musculoskeletal disease; immune disorder. High mobility group box; HMGB1; monoclonal antibody; antibody therapy

Homo sapiens ds sny

Rattus sp.

WO2005026209-A2.

24-MAR-2005

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Ношо варіепв
                                      Rattus sp.
                                                                                                                                                                                                                                                           Newman W,
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                                                                                                                                                                                                                                                                                                       The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of condition at sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB hox but does not binding fragment) binds to a vertebrate HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB correction. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pencreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1. An identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDXQPYEKKAAKLK 64
                                                                                                                                                                                New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High mobility group box; HMGB1; monoclonal antibody; antibody therapy; sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiarthmatic; lupus erythematosus; antiathmatic; lupus erythematosus; antiinflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 370; DB 9; Length 74; 100.0%; Pred. No. 4e-38; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2; 123pp; English.
                                                                                                             Okeefe T, Obar R;
                                                                        (CRIT-) CRITICAL THERAPEUTICS INC.
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                                    11-SEP-2003; 2003US-0502568P.
10-SEP-2004; 2004WO-US029527
                                                                                                                                                                                                                                             for treating, e.g. sepsis.
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                                                                                                                                               WPI; 2005-233483/24.
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Best Local Similarity
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                                                                                                             Qin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 74 AA;
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                                                                                                             Newman W,
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The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigential prind to non-A box epitopes of HMGB, and inhibits release of specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB protein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, pooriasis, partreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1. An identical sequence is also found in rat and mouse HMGB1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human high mobility group HMGB1 HMG-BOXB(large) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Obar R;
                                                                                                                                                                                                                                                                                                                                      (CRIT-) CRITICAL THERAPEUTICS INC.
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                                                                                                                                                                 10-SEP-2004; 2004WO-US029527
                                                                                                                                                                                                                                                                                                                                                                                                                     Okeefe T,
                                                                                                                                                                                                                                                   11-SEP-2003; 2003US-0502568P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating, e.g. sepsis.
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Matches 69; Conserv
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WO2005026209-A2
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                                                                                  24-MAR-2005
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The present invention relates to the use, especially in vitro, of nucleic acids encoding high mobility group proteins for the following processes: a magingenesis (including in a wound bed), neovascularization, transmyocardial revascularization, wound healing, epithelialization and healing in cases of tooth or bone implants. The sequences and their encoded protein are useful for treating a very wide range of diseases: (proliferation, athritis, endometriosis, histicotrosis, psoriasis, rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma, Kaposi sarcoma and basal cell carcinoma), haemorrhoids, atteriosclarosis, angina pectoris, ischaemia, infarction, infertility, wounds (including diabetic and other ulcers), also diseases associated with DNA damage, especially xeroderma pigmentosum, leather skin', skin cancers and ageing (including where associated with sunburn) and cardiac infarct, including cosmetic treatment, especially as a sun-protection composition. Compounds the protein and all the specified processes can also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                    Use of nucleic acids encoding basic DNA-binding proteins, and their translation or transcription products, for treating diseases associated with e.g. angiogenesis, neovascularization or wound healing, also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutically. The present sequence is a polypeptide of the invention.
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cardiant; vulnerary; antiulcer; high mobility group protein; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 370; DB 8; Length 75; 1 Similarity 100.0%; Pred. No. 4.1e-38; 69; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 57; SEQ ID NO 26; 161pp; German.
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                                                                                                                                                                                               07-MAR-2003; 2003DE-01010160.
10-AUG-2003; 2003DE-01036642.
08-OCT-2003; 2003DE-01046614.
                                                                                                                                              05-JAN-2004; 2004WO-EP000030
                                                                                                                                                                                    2003DE-01000023
                                                                                                                                                                                                                                                                          (ALCE-) ALCEDO BIOTECH GMBH.
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Best Local Similarity
Matches 69; Conserv
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                                                                         WO2004061456-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            screening
                                                                                                                                                                                                                                                                                                            Bullerdiek J;
                                         Homo sapiens
                                                                                                                                                                                  03-JAN-2003;
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                                                                                                            22-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                        New pharmaceutical composition comprises a polypeptide comprising an HMGB box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.
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HMGB B box; high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) B box biologically active fragment.
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100.0%; Pred. No. 5.1e-38;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                             (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 45; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO71534 standard; protein; 92 AA.
                                                                                                                                                                     19-NOV-2003; 2003WO-US036975.
                                                                                                                                                                                                          20-NOV-2002; 2002US-0427848P
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Les 69, Conservative
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                                                                                             WO2004046338-A2
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                                                          Homo sapiens.
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The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunesuppressive fragment of the vertebrate or non-natural HMGB A box. The immune pathology is induced by the administration of a non-human antigen, non-adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of individual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune pathology, inhibiting an immune pathology in an individual or decreasing an immune response to an administered non-human antigen comprise administering a HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural A box. A claimed method of treating an auto-maturally-occurring HMGB A cox, an on-naturally-occurring HMGB A box, an immunosuppressive fragment of these, and a vertebrate or non-naturally-occurring HMGB B cox, an immunosuppressive fragment of these, and a vertebrate or non-naturally-occurring HMGB C box, an immunosuppressive fragment of these, and a vertebrate or non-naturally-occurring HMGB C box, an immunosuppressive fragment of these and a vertebrate or non-naturally-occurring HMGB C box, an immunosuppressive fragment of these and a vertebrate or non-naturally-occurring HMGB C box, an immunosuppressive and a vertebrate or non-naturally-occurring HMGB continued the cleaning an element of these and a vertebrate or non-naturally-occurring HMGB continued the cleaning an element of these and a vertebrate or non-naturally-occurring HMGB continued to the cleaning an element of these and a vertebrate or non-naturally-occurring HMGB continued to the cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment.
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ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiashmatic; rheumatoid arthritis; antitheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAAADDKQPYEKKAAKLK
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(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 43; 57pp; English
                                                                                                                                                                                                                                                                                                                                10-SEP-2004; 2004WO-US029540,
                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2003; 2003US-0502349P.
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                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammaerory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB box but do not specifically bind to one. B proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the playpeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an useful in treating obesity and conditions characterised by activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, theumatorid arthritis, asthma, lugus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcer's disease, graft-vereus.host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB B box polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 58; 113pp; English.
                                                                                                                                                                                                                                                                                                 (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADY85368 standard; protein; 92 AA.
                                                                                                                                                20-NOV-2003; 2003WO-US037507.
                                                                                                                                                                                                        20-NOV-2002; 2002US-0427841P.
20-NOV-2002; 2002US-0427846P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69; Conservative
                                                                                                                                                                                                                                                                                                                                                            Newman W, O'keefe TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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EKYEKDIAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-420628/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                 WO2004046345-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92 AA;
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High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                             sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antiatthritic; asthma; antiathmatic; lupus erythematosus; antiatthritic; asthma; antiathmatic; lupus erythematosus; antiantlammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; asstrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Obar R;
ADY85084 standard; protein; 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                       (CRIT-) CRITICAL THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Okeefe T,
                                                                                                                                                                                                                                                                                                                                                    10-SEP-2004; 2004WO-US029527
                                                                                                                                                                                                                                                                                                                                                                              11-SEP-2003; 2003US-0502568P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating, e.g. sepsis.
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-233483/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Qin S,
                                                                           Human HMGB1 A box
                                                                                                                                                                                                                                                                                                 WO2005026209-A2
                                                                                                                                                                                                                                               Homo sapiens
                                                 16-JUN-2005
                                                                                                                                                                                                                                                                                                                            24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                Newman W,
                                                                                                                                                                                                                                                              Mus sp.
Rattus sp.
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The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB A box but does not binding fragment) binds to a vertebrate HMGB A box but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB protein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndromic obstructive pulmonary disease, psoriasis, peniconitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, arthritis, and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1. ANY85012. An identical
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                                                                                    NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLIK
                                                                   NAPKRPPSAFFLFCSEYRPKI KGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                  Gaps
                                  ;
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   Length 92;
                                  0; Indels
100.0%; Score 370; DB 9;
100.0%; Pred. No. 5.1e-38;
iive 0; Mismatches 0;
               Local Similarity 100.
es 69; Conservative
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 Query Match
                                  Matches
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Length 128; Indels

100.0%; Score 370; DB 3; 100.0%; Pred. No. 7.6e-38; ive 0; Mismatches 0;

Best Local Similarity 100. Matches 69; Conservative

Query Match

Sequence 128 AA;

9 69

10 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEKKAAKLK 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK

61 EKYEKDIAA 69

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Human, prostate cancer, prostate cancer antigen, detection, diagnosis, neuroprotective; cytostatic, cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           issociated gene sequences, referred to as prostate cancer for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                  Human prostate cancer antigen protein sequence SEQ ID NO:1757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 2225-2226; 2338pp; English
                                                                                                                          AAB57179 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US005988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate cancer associated antigens, useful for treatm
                                                                                                                                                                                                13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as prostate cancer
69
                              73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Ruben SM;
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                            EKYEKDIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF16382
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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us-10-717-984-5.rag

EKYEKDIAA 78

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Tumour-associated antigenic target (TAT) polypeptide PRO82460, SEQ:4238. Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or Claim 12; SEQ ID NO 4238; 7273pp; English. ABM81641 standard; protein; 168 AA. 29-SEP-2003; 2003WO-US028547. 02-OCT-2002; 2002US-0414971P. (first entry) Wu TD, Zhang Z, Zhou Y; gene therapy; cytostatic. prostate cancer or tumor. (GETH) GENENTECH INC. WPI; 2004-347921/32. N-PSDB; ACN39840 Sequence 168 AA; WO2004030615-A2 ношо варіепв 18-NOV-2004 15-APR-2004. ABM81641; RESULT 15 **ABM8164**

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide and polypeptides at least 80% identical to the TAT nucleic acids and polypeptides appetides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; a peptide or organic acid; an antibody specific for a TAT polypeptide; and retroads and compositions for the treatment or diagnosing of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, nung cancer, cervical cancer, cancers of the central used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence 100.0%; Score 370; DB 8; Length 168; 100.0%; Pred. No. 1e-37; Live 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 69; Conservative

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Gaps ö

61 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWINTAADDKQPYEKKAAKLK 120 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 60 셤 ò

69 61 EKYEKDIAA g

121 EKYEKDIAA 129

6, 2006, 10:19:12 Search completed: April Job time: 83.7533 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                      Copyright
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OM protein - protein search, using sw model

6 April ü 0 Run

2006, 10:19:38 ; Search time 13.1645 Seconds (without alignments) 504.309 Million cell updates/sec

US-10-717-984-5 Title: Perfect score:

1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

piri:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		nonhistone chromos	nonhistone chromos	nonhistone chromos	non-histone chromo	nonhistone chromos	nonhistone chromos	high mobility grou	nonhistone chromos			nonhistone chromos	high-mobility grou	high mobility grou	nonhistone chromos		HMG-1 - chicken	nonhistone chromos	high mobility grou	nonhistone chromos	nonhistone chromos	gene HMG-T2 protei	DNA-binding protei	structure-specific	high mobility grou	high mobility grou	HMG1 protein - sea	dorsal switch prot	nonhistone chromos
SUMMARIES	ΙD	A27853	NSRTH1	S01947	802826	148688	A28897	S29857	862355	S30221	NSHUH2	A34719	JC1129	JC1114	S54774	A24019	S48708	I50254	\$22359	T01071	S26062	B61611	151067	A41265	A41976	T03374	878050	JC4357	617	820068
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	Length	170	215	215	215	215	215	216	210	186	209	210	207	207	210	172	204	201	202	204	205	186	215	708	709	138	699	200	393	393
di	Query Match	100.0	100.0	100.0	100.0	100.0	98.6		90.5	87.6	87.6	87.6	86.8	86.2	85.4	81.4	81.4	81.1	81.1		79.5	78.9	71.1	46.5	45.9	45.5	45.4	44.9	44.9	44.9
	Score	370	370	370	370	370	365	360	335	324	324	324	321	319	316	301	301	300	300	298	294	292	263	172	170	168.5	168	166	166	166
	Result No.	7	7	Э	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		29

probable high mobi	high mobility grou	nonhistone chromos	high mobility grou		high mobility grou	scription	mobility	mobility	mobility	high mobility grou	mobility	HMG protein [impor	nonhistone chromos	high mobility grou	high mobility grou
T09581	S35637	A35072	\$39556	T03372	T07377	T12113	B47150	S18991	T03640	T02252	S40302	T51159	S78076	T03375	T51598
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141 2	561 2	~	149 2	139 2	141 2	642 2	157 2	7	7	142 2	7	178 2	99 2	126 2	141 2
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44.5	561 2	44.1 93 2	43.9	43.4		43.0	42.8	42.8 161 2	42.8 168 2	42.6	42.6 144 2	42.3			

ALIGNMENTS

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CiAccession: A27853
Rilee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A; Title: Characterization of cDNA sequences corresponding to three distinct HWG-1 mRNA signification at the contemporary of the contemporary 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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1es 69; Conservative
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~ RESULT

nonhistone chromosomal protein HMG-1 - rat
NyAlternate names: 30K heparin-binding protein, brain; amphoterin
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Date: 1922 Resquence revision 31-Dec-1992 #text change 09-Jul-2004
Cisacession: A41175; A27298; A30188; B48771; A48771; C48771
R;Meremmies, J; Pihlaskari, R; Laitinen, J; Wartiovaara, J; Rauvala, H.
J; Biol. Chem. 266, 16722-16729, 1991
A;ritle: 30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgro

A, Accession: A41175 A, Molecule type: mRNA A, Residues: 1-215 <MER>

A;Cross-references: UNIRKOT:P07155; UNIPARC:UPI0000008A6; GB:M64986; NID:g202884; PIDN:. A;Note: part of this sequence, including the amino end of the mature protein, was confir. A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in

h-mobility group proteins R; Paonessa, G.; Frank, R.; Cortese, Nucleic Acids Res. 15, 9077, 1987

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Gaps

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A; Molecule type: protein
A; Mesidues: 2-22, X', 24.38 cGHR>
A; Cross-references uniparc: UP10000173989
A; Cross-references uniparc: UP10000173989
B; Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A; Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group, A; Reference number: 145910
A; Reference number: 145910
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 'PGG', 119, 'V', 121-215 cPEN>
A; Ross-references: UNIPARC: UP100016C31E; GB:M26110; NID:g163156; PIDN:AAA30567.1; PID:g. C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Reywords: chromosomal protein; DNA binding; duplication; nucleus
F; 2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted cMAT>
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A;Molecule type: mRNA
A;Residues: 1-215 <WEND
A;Residues: 1-215 <WEND
A;Cross-references: UNIPROT: P09429; UNIPARC: UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Blectrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma prot
A;Reference number: A33178; MUID:91176935; PMID:2079031
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C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: 802826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
A;Ciele: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: 802826; MUID:89160247; PMID:2922262
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A; Molecule type: protein
A; Residues: 2-13, 'XXF' < WAR>
A; Cross-references: UNIPARC: UP100001771D7
A; Accession: G33178
A; Molecule type: protein
A; Residues: 2-13, 'XX', 16-22 < WA2>
C; Genetics:
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F;92-166/Domain: HMG box homology <HMG2>
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ilarity 100.0%;
Conservative 0
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Matches 69; Conserv
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solidary 3
nonhistone chromosomal protein HMG-1 - bovine
NyAlternate names: 33K protein, high-mobility-group protein HMG-1
C;Species: 30.5ep-1989 #sequence_revision_22-Apr-1995 #text_change 09-Jul-2004
C;Apccession: 501947; A61611, 510959; 145910
C;Apccession: 501947; A61611, 510959; 145910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length CDNA sequence for bovine high mobility group 1 (HMG1) protein.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length CDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: 501947; MUID:89057489; PMID:3194213
A;Accession: 501947
A;Molecule type: mRNA
A;Residues: 1-21s cKAPP
A;Cross-references: UNIPROT:P10103; UNIPARC:UP1000016C31D; EMBL:X12796; NID:9416; PIDN:C
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FEBS: Lett. 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Recidues: 2-22, 'S, '24-40;48-105,'A', 107-157,'X', 160-193,'D', 195 <WAL>
A;Rossidues: 2-22, 'S, '24-40;48-105,'A', 107-157,'X', 10
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Kossicule type: protein
A;Kossicule type: protein
A;Kossicule type: protein
A;Kossicule type: protein
A;Crossicule type: protein
A;Crossicule type: protein
A;Crossicule type: protein
A;Crossicule type: A; Molecule type: A; Raulo, B; Molecule type: A; Mole
     A; Title: Nucleotide sequence of rat liver HMC1 cDNA.
A; Reference number: A27298; MUID:88067717; PMID:3684582
A; Accession: A27298
A; Accession: A27298
A; Molecule type: mRNA
A; Residues: 1-10, "R',12-82,84-95,97, "AS',100-215 <PAO>
A; Cross-references: UNIPARC:UP10000173984
B; Rauvala, H.; Merenmies, J.; Philaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P. J. Call Biol. 107, 2293-2305, 1988
A; Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 98-105, X', 107-112 cPA2>
A;Cross-references: UNIPARC:UPI0000173986
A;Cross-references: UNIPARC:UPI0000173986
A;Cross-references: UNIPARC:UPI0000173986
A;Cross-reference cource: postnatal brain
A;Note: sequence extracted from NCBI backbone (NCBIP:137788)
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
E;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental cMAT>
F;6-83/Domain: HMG box homology cHMG-2
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ive 0; Mismatches
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A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Superfamily: norhistone chromosomal protein; DNA binding; nucleus
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
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A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI A;Note: the authors did not translate the codon for residue 1 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein F;6-83/Domain: HMG box homology <HMG1>
F;6-83/Domain: HMG box homology <HMG2>
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A;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>
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Rividatingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
A; Title: Evidence for a shared structural role for HWG1 and linker histones B4 and A; Reference number: S62355; WUID:96174815; PMID:8599938
A; Accession: S62355
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C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S2981
R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
A;Accession: S29857
A;Status: preliminary
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C;Species: Xenopus Laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 862355
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DMA binding; nucleus F;6-83/Domain: HMG box homology cHMG1> F;92-166/Domain: HMG box homology cHMG2>
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A;Residues: 1-210 <NIG>
                                                                                                                                                                      'Match 98.6%; Score 365; DB 2; Local Similarity 98.6%; Pred. No. 1.7e-32; les 68; Conservative 0; Mismatches 1;
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Pred. No. 6.1e-32;
0; Mismatches 1
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Best Local Similarity 98.6%;
Matches 68; Conservative (
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|153 EKYEKDIAA 161
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                                                                                                                                                                          Query Match
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                                                                                                                                                                                        RESULT 5
148688
non-histone chromosomal high-mobility group 1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148689; A55402; T57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Accession: 148688
A;Accession: 148688
A;Reference number: AREA
A;Molecule type: mRNA
A;References: UNIPROT:P07155; UNIPARC:UP100000008A6; EMBL:Z11997; NID:953381; PIDN
B;Perrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808; 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402
A;Crossion: A55402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189, E', 191-215 - FERE
A;Crossereferences: UNIPARC:UP1000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
B;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Mamm: Genome 5, 91-99, 1994
A;Title: The mouse coding for high mobility droup 1 protein (HMG1).
A;Residues: 1-189, E', 191-215, FERE
A;Crossereferences: UNIPARC:UP1000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
A;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
A;Title: And A; And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ведиел
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R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide A;Reference number: A28897; MUD:89050965; PMID:3191113
A;Rocession: A28897
A;Rocession: A28897
A;Rolecule type: mRNA
A;Residues: 1-215 <TSU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
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A;Reference number: 157021; MUID:94235965; PMID:8180479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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100.0%; Pred. No. 4.9e-33;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: 157021
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: nonhistone chromosomal pro
C; Keywords: chromosomal protein
F; 6-83/Domain: HMG box homology <HMG1>
F; 92-166/Domain: HMG box homology <HMG2>
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                                                                              FKYEKDIAA 161
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                                       EKYEKDIAA
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Best Local Similarity
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C;Accession: A34719 Teuda, K.; Yoshida, M. B;Accession: A34719 MID:90275208 Protein HMG2 revealed by the nucleu A;Reference number: A34719; MUID:90275208; PMID:2350545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UP1000016C6C5; GB:J02895; NID:g164491; PIDN:F:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
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F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
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C;Species: Gallus gallus (chicken)
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
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R;Sparrow, D.B.; Wells, J.R.E.
Gene 114, 289-290, 1992
A;Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2. A;Reference number: JC1129; MUID:92290291; PMID:1601311
A;Accession: JC1129
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A;Map position: 7pter-7qter
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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87.0%; Pred. No. 5.1e-28;
ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 207;
                                                                                                                                                                                                Length 209,
                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                   DB 1;
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Pred. No. 5e-28;
4; Mismatches

    chicken

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Best Local Similarity 87.0%;
Matches 60; Conservative
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153 EKYEKDIAA 161
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A; Residues: 1-207 <SPA>
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Matches
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NGHUHZ

Conhistone chromosomal protein HMG-2 - human

Cispeciae: Homo sapiens (man)

Cispeciae: Homo sapiens (man)

Cispeciae: Homo sapiens (man)

Cispeciae: Homo sapiens (man)

Cispeciae: Homo sapiens

Cipate: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004

Cispeciae: Homo sapiens

Cispeciae: A2425; S20061; S18068

Rishirakawa, H.; Yoshida, M.

J. Biol. Chem. 267, 6641-6645, 1992

A;Title: Structure of a gene coding for human HMG2 protein.

A;Reference number: A42425; MUID:92202209; PMID:1551873

A;Recession: A42425

A;Molecule type: DNA

A;Residues: 2-209 < KHIS

A;Residues: Visit of the homo NCBI backbone (NCBIN:89899; NCBIP:89900)

A;Note: sequence extracted from NCBI backbone (NCBIN:89899; NCBIP:89900)

A;Note: initiator Met not shown

R;Moludar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M.

Nucleic Acids Res. 19, 6643, 1991

A;Title: Sequence of human HMG2 CDNA.

A;Reference number: S20061; MUID:92093633; PMID:1754403

A;Recession: S20061

A;Molecule type: mRNA

A;Residues: 1-209 < KAAJ>

A;Coss-references: UNIPARC:UPI000013834D; EMBL:X62534; NID:932332; PIDN:CAA44395.1; PID

C;Genetics:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:217240; NID:332334; PIDN A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords cromosomal protein protein chromosomal protein HMG-2; HMG box homology (F:1-60)Domain: HMG box homology (fragment) <HMG>
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                                                                                                                                      70 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEGSAKDKQPYEQKAAKLK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S30221
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-186 <ALE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S3021,
Nucleic Acids Res. 20, 6413, 1992
A;Title: A human HMG2 cDNA with a novel 3'-untranslated region.
A;Reference number: S30221; MUD:93117123; PMID:1475204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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Pred. No. 4.4e-28;
4; Mismatches 5; Indels
   | Similarity 85.5%; Pred. No. 3.2e-29; 59; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonhistone chromosomal protein HMG-2B - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: GDB:NHCP2
A,Cross-references: GDB:119451; OMIM:118880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vuery march
Best Local Similarity 87.0%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                   130 EKYEKDIAA 138
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                                                                                                                                                                                                                                  EKYEKDIAA 69
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKYEKDIAA
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85.5%;

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NyAlternate names: HWG-T
C;Species: Salmo sp. (trout)
C;Species: Salmo sp. (trout)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24019
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Axicle: Acida Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high A;Reference number: A24019; WUID:85269614; PMID:4022777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NAPKRPSSAFFIFCADFRPQVKGETPGLSIGDVAKKLGEKMNNLTAEDKVPYEKKASKLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P07746; UNIPARC:UP100001771D6
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: Chromosomal protein; DNA binding; nucleus
F;1-50/Domain: HMG box homology (fragment) <HMG1>
F;59-133/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
81.4%; Score 301; DB 2; Length 172;
Best Local Similarity 78.3%; Pred. No. 1.3e-25;
Matches 54; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                         nonhistone chromosomal protein HMG-T - trout (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6, 2006, 10:26:19
                            153 EKYEKDIAA 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A24019
A;Molecule type: mRNA
A;Residues: 1-172 <PEN>
                                                                                                                                                                A24019
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                                                                                                                                                                                                                                                                                                                                                                                                                                high-mobility group protein 2 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: JC1114
R;Davis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt A;Reference number: JC1114; MUID:92241676; PMID:1572546
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C;Species: Mus musculus (house mouse)
C;Species: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of A;Reference number: S54774; MUID:95237201; PMID:7720710
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                                                                                                                                   93 NAPKRPPSAFFLFCSEHRPKIKNDHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 152
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                                   0; Gaps
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                                   Indels
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Pred. No. 1.1e-27;
5; Mismatches 5
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Pred. No. 3.8e-27;
3; Mismatches 6;
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F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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Best Local Similarity 87.0%;
Matches 60; Conservative
                                      59; Conservative
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153 EKYEKDIAA 161
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   Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-207 < DAV>
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us-10-717-984-5.rup

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GenCore version 5.1.7
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Copyright (c) 1993 - 2006 Biocceleration Ltd.	model	April 6, 2006, 10:13:48; Search time 81.4836 Seconds (without alignments) 597.439 Million cell updates/sec	
Copyright (c)	OM protein - protein search, using sw model	April 6, 2006,	
	OM protein .	Run on:	

Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA 69

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8c7c4 mus musculu	P07156 cricetulus	Q8bnm0 mus musculu	Q5t7c5 homo sapien	P10103 bos taurus	Q6yka4 canis famil	P09429 homo sapien	P63158 mus musculu	P63159 rattus norv	Q5t7c3 homo sapien							m high	gallus	gallus	sus (Q14321 homo sapien	แนย	ម្ហាយ	Q5bkq1 mus musculu	Q9ugv6 homo sapien	Q9ngj4 homo sapien	Q5t7c2 homo sapien	Q5t7c4 homo sapien	Q59gwl homo sapien	xenopus	Q7sz42 xenopus lae
SUMMARIES	ID	C	HMG1_CRIGR	Q8BNMO MOUSE	QST7CS_HUMAN	HMG1 BOVIN	HMG1_CANFA	HMG1 HUMAN	HMG1_MOUSE	HMG1_RAT	QST7C3_HUMAN	Q4R844 MACFA	088611_SPAEH	O88612_SPAEH	O9QWY6_SPAEH	Q9QX40_SPAEH	Q548R9_RAT	Q58EV5_MOUSE	Q9PUK9 CHICK	Q9YH06_CHICK	HMG1_PIG	Q14321 HUMAN	Q6P202_MOUSE	Q8BQ02_MOUSE	Q5BKQ1 MOUSE	HMG1X_HUMAN	Q9NQJ4_HUMAN	Q5T7C2 HUMAN		Q59GW1 HUMAN		Q7SZ42_XENLA
	9B	~		•	~	н	н	Н	н	П	•		~	7	7	7	7	~	0	7	-	7	~	7					7		7	~
	Length	1	180	181	192	214	214	214	214	214	215	215	215	215	215	215	215	215	214	215	214	215	215	215	206	211	211	157	158	176		211
d	Query Match	100	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.9	98.9	98.6	98.6	œ.				'n.		95.1		92.2	91.1
	Score	1	370	370	370	370	370	370	370	370	370	370	370	370	370	370	370	370	366	366	365	365	364	360	359	356	355	352	352	352	341	337
	Result No.	-	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22			25	56	27		29	30	31

Q91596 xenopus lae Q6qnq5 xenopus lae	Q96j53 homo sapien P26583 homo sapien	Q5u071 homo sapien P17741 sus scrofa	P52925 rattus norv	Q5u072 homo sapien	Q5fvp0 rattus norv	Q9n1q5 hylobates l	Q8ch24 mus musculu	Q6y235 pagrus majo	P26584 gallus gall	Q9n1q7 pan troglod
Q91596_XENLA Q6GNQ5_XENLA	Q96J53 HUMAN HMG2 HUMAN	Q5U071 HUMAN HMG2 PIG	HMG2_RAT	Q5U072 HUMAN	Q5FVP0_RAT	SP100 HYLLA	Q8CH24 MOUSE	Q6Y235 PAGMA	HMG2 CHICK	SP100_PANTR
0 0	7 7	7 7	-	~	N	Н	~	7	Н	н
210	195 208	208	209	209	210	242	199	200	206	215
90.5	87.6 87.6	87.6	9.78	87.6	87.6	87.6	87.4	86.2	86.2	86.2
335 335	324 324	324 324	324	324	324	324	323.5	319	319	319
32 33	3.4 3.5	36 37	38	39	40	41	42	43	44	45

ALIGNMENTS

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CRIGR
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Hanagaki T., Haracka T., Hirozane T.,
Hayashida K., Hayatsu W., Hirancto K., Hiracka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Konno H., Konno H., Konno H.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki K., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AKOSOGS9, BACJAJS7.1; -; mRNA.
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                                                                                            Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wuramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                   MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Nagada K., Nagada K., Nagada K., Nagada K., Nagada M., Titoh M., Aizawa K., Nagada T., Tashiro H., Itoh M., Sumi N., Ishii K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mataumoto H., Sakaguchi S., Inkegami T., Kashiwagi K., Fujiwake S., Inoue K., Tozawa K., Tanaka M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riki integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI; MGI:96113; Hmgbl.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; F:nucleus; TAS.

GO; GO:0005515; F:nucleus ing; IPI.

GO; GO:0006610; P:transport; IDA.

GO; GO:0006610; P:transport; IDA.

InterPro; IPR000135; Highmobity_12.

InterPro; IPR000115; HMG_12_box.
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                                                        STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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100.0%; Pred. No. 1.4e-31;
ive 0; Mismatches 0;
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SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
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Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00505; HMG box;
PRINTS; PR00886; HIGHMOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKYEKDIAA 161
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NUCLEOTIDE SEQUENCE.
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RESULT 🏖

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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GO; GO:0005288; P:base-excision repair, DNA ligation; ISS.
GO; GO:0006210; P:DNA recombination; ISS.
GO; GO:0006281; P:DNA repair; ISS.
GO; GO:0006281; P:DNA unwinding; ISS.
GO; GO:0006228; P:Establishment and/or maintenance of chromat. . .; ISS.
GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
InterPro; IPR000135; Highmoblty_12.
PitterPro; IPR000130; HMG 12 box.
Pfam; PF00505; HMG box; Z.
PRINTS; PR00866; HIGHMOBLTX12.
                                                                                 01-APR-1988 (Rel. 07, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein B1)
                                                                                                                                                                              (Fragment).
Name=HMGB1; Synonyms=HMG-1, HMG1;
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Bubneria; Craniata; Vertebrata; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93347974; PubMed=8346022; Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.; "Solution structure of a DNA-binding domain from HMG1."; Nucleic Acids Res. 21:3427-3436(1993).

-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle expression of the HMG-1 gene."; Nucleic Acids Res. 15:5051-5068(1987).
                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=87259986; PubMed=3601666;
Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX-2; 2.
3D-structure; Chromosomal protein; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-1- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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HMG box 2.
Asp/Glu-rich (acidic).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0000793; C:condensed chromosome; ISS. GO:0008301; F:DNA bending activity; ISS.
180 AA.
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PIR; A27853; A27853.
                                                           01-APR-1988 (Rel. 07, Created)
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PDB; 1HSN; NWR; @=58-136.
PDB; 1NHM; NWR; @=58-136.
PDB; 1NHN; NWR; @=58-136.
   STANDARD;
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151
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83
87
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QST7CS_HUMAN
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                                                                                                                                                                                                                                                58 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKOPYEKKAAKLK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430013M12 product:high mobility group box 1, full
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                  1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota; Metazao; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murines; Mus.
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279553; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                        ;
0
                                                                                                                       Length 180;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                      0; Indels
97
100
128
20904 MW; F624392F41609854 CRC64;
                                                                                                                       100.0%; Score 370; DB 1; 100.0%; Pred. No. 1.4e-31;
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                                                                                                                                                                      0; Mismatches
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence. (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBBNMO_MOUSE PRELIMINARY;
QBBNMO;
                                                                                                                                                                      69; Conservative
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                                                                                                                                                                                                                                                                                                                                                             118 EKYEKDIAA 126
                                                                                                                                                                                                                                                                                                                   61 EKYEKDIAA 69
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                                                                       180 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CSTBL/61; TISSUE-Whole body;
Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Hashizume W.,
Pukuda S., Furuno M., Hanagaki T., Haraoka T., Hirożane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa T., Hirożane T.,
A Hari F., Imotani K., Ishii Y., Itoh M., Kagawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kowa M., Koya S.,
A Kutihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakazuwe N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
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                             MEDLINE=20499374; PubMed=11042155; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Nuramatsu M., Hayashizaki Y., Incheration of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MGI; MGI:96113; Hmgbl.

MGI; MGI:96113; Hmgbl.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; C:intracellular space; IDA.

GO; GO:0005515; F:nitric-oxide synthase regulator activity; IDA.

GO; GO:0006515; F:protein binding; IPI.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

InterPro; IPR000113; Highmoblty_12.

InterPro; IPR000910; HMG loox; Z.

Pfam; PF006905; HMG box; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 1.4e-31;
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100.0%; Score 370; Di
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 69; Conservative 0; Mismatches
STRAIN=C57BL/6J; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00353; HMG BOX 1; 1. PROSITE; PS50118; HMG BOX 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00505; HMG box; Z. PRINTS; PR00886; HIGHMOBLTY12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||
153 EKYEKDIAA 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P07156; 1NHN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                        A belan S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

B BMBL; Al353649; CAI15602.1; -; Genomic_DNA.

B MRI, OST7C5; 2-84, 93-171.

R GO; GO:0000785; C:chromatin; IEA.

GO; GO:000587; F:nucleus; IEA.

GO; GO:0003677; F:nw binding; IEA.

GO; GO:0003677; F:nw binding; IEA.

GO; GO:0003677; F:nw binding; IEA.

DR HINEYED: PRO00135; Highmobity_12.

DR PRINTS; PRO0086; Highmobity_12.

DR PRINTS; PRO0086; Highmobity_12.

DR PRINTS; RRO0866; Highmobity_12.

DR PROSITE; PSO0353; HMG; 2.

DR PROSITE; PSO0353; HMG BOX_1; 1.

DR PROSITE; PSO0118; HMG BOX_2; 2.

FT NON_TER.

FT NON_TER.
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HWG1_BOVIN STANDARD; PRT; 214 AA.
P1013;
01-MAR-1989 (Rel. 10, Created)
01-MAG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pentecost B., Dixon G.H.;
"Isolation and partial sequence of bovine cDNA clones for the high-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Holstein, TISSUE=Fetal thymus;
MEDLINES=89657489; PubMed=3194213;
Kaplan D.J., Duncan C.H.
"Full length cDNA sequence for bovine high mobility group 1 (HMG1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=HMGB1; Synonyms=HMG1;
Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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                                     01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment).
Name=HMGB1; ORFNames=RP11-550P23.1-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 370; DB 2;
100.0%; Pred. No. 1.5e-31;
iive 0; Mismatches 0;
192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 16:10375-10375(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
MEDLINE=84128872; PubMed=6141822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
NUCLEOTIDE SEQUENCE [MRNA].
QST7CS HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKYEKDIAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKYEKDIAA 69
                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
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S MAK; F10103; 1-63, 2-1.70.

R GO; GO:0000793; C:condensed chromosome; ISS.

R GO; GO:0000793; C:condensed chromosome; ISS.

R GO; GO:0006289; F:DNA bending activity; ISS.

R GO; GO:0006289; P:base-excision repair, DNA ligation; ISS.

R GO; GO:0006281; F:DNA recombination; ISS.

R GO; GO:0006281; P:DNA recombination; ISS.

R GO; GO:0006281; P:DNA recombination; ISS.

R GO; GO:0006281; P:DNA unwinding; ISS.

R GO; GO:0006282; P:establishment and/or maintenance of chromat. .; ISS.

R GO; GO:0006282; P:establishment and/or maintenance of chromat. .; ISS.

R GO; GO:0006325; HRG box; Z.

R InterPro; IPR000310; HRG 12 box.

R Pfan; PR00816; HRG box; Z.

R RNART; RN00398; HNG; 2.

R ROSITE; PS00185; HNG BOX 1; 1.

R ROSITE; PS00185; HNG BOX 1; 1.

R ROSITE; PS00185; HNG BOX 2; Z.

CHROMOSOMAI Protein; Repeat. This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not ö 92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 151 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK MEDLINE=81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4; Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.; "The primary structures of non-histone chromosomal proteins HMG 1 and 0; Gaps PROJECT STATE TO STATE STAT 100.0%; Score 370; DB 1; Length 214; 100.0%; Pred. No. 1.7e-31; ive 0; Mismatches 0; Indels C -> S (in Ref. 3). C -> A (in Ref. 3). EHPGL -> PGGGV (in Ref. 2). E -> D (in Ref. 3). B 253A80FC7P0P433 CRC64; Asp/Glu-rich (acidic). PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194. HMG box 1. EMBL; X12796; CAA31284.1; -; mRNA. EMBL; M26110; AAA30567.1; -; mRNA. PIR; S01947; S01947. HSSP; P07156; INHN. SWR; P10103; 1-83, 92-170. mobility-group protein (HMG-1)."; 162 HG 214 As 22 C 105 C 119 EI 193 E FEBS Lett. 122:264-270(1980). Biosci. Rep. 4:49-57(1984) PROTEIN SEQUENCE OF 1-36. 69; Conservative 152 EKYEKDIAA 160 61 EKYEKDIAA 69 22 105 115 193 214 AA; Similarity

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMED outstation the Buropean Bloinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                            10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytogenet. Genome Res. 101:33-38(2003).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;
Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 370; DB 1; Length 214; 100.0%; Pred. No. 1.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 0 By similarity.
8 78 HMG box 1.
94 162 HMG box 2.
185 214 AspyClu-rich (acidic).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murua Escobar H., Meyer B., Richter A., Becker K., Bullerdiek J., Nolte I.; "Molecular characterization of the canine HMGBL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY135519; AAN11296.1; -; mRNA.
EMBL; AY135521; AAN11319.1; -; Genomic_DNA.
HSSP; POT155; 1AAB.
HSS ; QGYXA4; 1-83, 92-170.
Ensembl; ENSCAFG0000006597; Canis familiaris.
                                                                      214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. nc.
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InterPro; IPR000910; HMG 12 box.
Pfan; PR00505; HMG box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Conservative
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||||
152 EKYEKDIAA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                      Name=HMGB1;
                                                                      CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
COMPBIAS
SEQUENCE
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DNA_BIND
                                                                   HMG1 CAN
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HWG1 CANFA

TO MAGY CA

AC OGYKAA,

DT 10-MAY.

DT 10-MAY.

DE High mc

B B1).

GN Name=H

OC Canis

OC Canis

OC Canis

OC Canis

CC Canis

RA MULLIN

RA MULLIN

RA MUCLEO

RA MUCLEO

CC Canis

CC Canis

CC Canis

CC Canis

CC Canis

DC CANIS

RA MULLIN

RA MULLIN

RA MULLIN

RA MULLIN

CC Canis

CC Cani
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HMG1 HUMAN
ID HMG1 H1
AC P09429
DT 01-MAR
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214 AA

PRT;

HMG1 HUMAN STANDARD; P09429; Q61BE1; 01-MAR-1989 (Rel. 10, Created)

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TISSUE-Brain, Cervix, and Testies Factors of Carubourder Succession of Cervix, and Testies of Carubourder Succession of Cervix, and Testies of Carubourder S. Peingold B.A., Grouse L.H., Derge J.G., Median R.B., Collins F.S., Magner L., Schaefer C.F., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Brankeron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Morean R.J., Malek J.A., Guaratane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rabey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abutting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Sheviguez A., Schmutz J., Myers R.M., Schein J.B., Jones S.J., Warra M.A., Richertield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., Touchman J.W., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.M., Marra M.A., Schein J.B., Jones J.
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bbert L., Schick M., Newbert P., Schatten R., Henze S., Korn B.;
"Cloning of human full open reading frames in Gateway(TM) system entry
vector (pDONR201).";
01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369; Perraris S., Finelli P., Rocchi M., Bianchi M.E., "The active gene that encodes high mobility group 1 protein (HMG1) contains introns and maps to chromosome 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S. Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y. Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) system donor
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA].
MUDLINES 89160247; PubMed=2922262;
Wen L., Huang J.K., Phohnson B.H., Reeck G.R.;
"A human placental cDNA clone that encodes nonhistone chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE [MRNA].
He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The German cDNA consortium; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 57-64 AND 112-126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 17:1197-1214(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 35:367-371(1996).
                                                                                                                 Name=HMGB1; Synonyms=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Small intestine;
                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                 protein HMG-1."
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NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                            HMG1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, 163905; -. Geondensed chromosome; IDA.
GO:0008301; F:DNA bending activity; TAS.
GO:0008134; F:transcription factor binding; TAS.
GO:0006288; P:DNA excembination; TAS.
GO:0006281; P:DNA recombination; TAS.
GO:0006281; P:DNA unvinding; NAS.
GO:00062825; P:DNA unvinding; NAS.
GO:0006285; P:DNA unvinding; NAS.
GO:0006255; P:establishment and/or maintenance of chromat. .; TAS.
GO:0017055; P:negative regulation of transcriptional pred. .; IDA.
GO:0006357; P:regulation of transcription from RNA polyme. .; IDA.
                    Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
Simpson R.J., Dorow D.S.;
Simpson R.J. and the second s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein; Direct protein sequencing; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                               P04637:TP53; NDExp=1; IntAct=EBI-389432, EBI-3866083; O15350:TP73; NDExp=1; IntAct=EBI-389432, EBI-389606; -: SUBCELLULAR LOCATION: Nuclear.
-: SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-: SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asp/Glu-rich (acidic).
E -> D (in Ref. 5).
B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 370; DB 1; 100.0%; Pred. No. 1.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X12597; CAA31110.1; -; mRNA.
EMBL, U31677; AAB08987.1; -; Genomic_DNA.
EMBL, AY377859; AAQ91389.1; -; mRNA.
EMBL, CR749614; CAH18408.1; -; mRNA.
EMBL, CR456863; CAG33144.1; -; mRNA.
EMBL, BT006940; AAP35866.1; -; mRNA.
EMBL, BC003378; AAV38961.1; -; mRNA.
EMBL, BC003378; AAH03378.1; -; mRNA.
EMBL, BC066889; AAH6889.1; -; mRNA.
EMBL, BC066889; AAH6889.1; -; mRNA.
EMBL, BC066889; AAH66889.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG 12_box.
InterPro; IPR000910; HMG 12_box.
Edm; PP00105; HMG_box; Z.
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S02826; S02826.
HSSP; P07156; 1NHN.
SMR; P09429; 1-83, 92-170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC; HGNC: 4983; HMGB1.
H-InvDB; HIX0011209; -.
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GO; GO:0000134

GO; GO:0008134

GO; GO:0006218

GO; GO:0006218

GO; GO:0006218

GO; GO:0006218

GO; GO:0006228

GO; GO:0006228

GO; GO:0006325

GO; GO:0006325
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl;
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SOLUTION TO THE TELEFICION OF THE PROPERTY OF
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Gaps

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0; Indels

0; Mismatches

69; Conservative

Matches

Local Similarity

1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

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REAL NUCLILUE SEQUENCE LIMANOS DICALE FROMENTA
RAY REDLINE-22388257; PubbMed=12477932; DOI=10.1073/pnas.242603899;
RAY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Wagner L., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Farner C.R.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schein J.S., Nor. Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.
92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
Pauken C.M., Magle D.L., Bucan M., Lo C.W.;
"Molecular cloning, expression analysis, and chromosomal localization of mouse Hmgl-containing sequences.";
Manm. Genome 5:91-99(1994).
                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazaa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                             HMG1 MOUSE STANDARD; PRT; 214 AA. P61158; P07155; P27109; P27428; P61158; P07155; P27109; P27428; P61158; P07155; P27109; P27428; P61158; P071621992 (Rel. 23, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yotov W.V., St Arnaud R.; "Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group protein-1 (HMG1)."; Nucleic Acids Res. 20:3516-3516(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ghosh B.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92335012; PubMed=1630928;
                                                                                               152 EKYEKDIAA 160
                                                             69
                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
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                                                             61 EKYEKDIAA
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C3H/He;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AKR/J;
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EMBL; M64986; AAA40729.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 12:1311-1319(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 1-83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 1-20.
      norvegicus (Rat)
                                                                                                                                                                                                     SEQUENCE REVISION.
                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panula P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    removed.
    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P63159; P07155; P27109; P27428; 01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) High mobility group protein 1 (HMG-1) (High mobility group protein B1) (Amphoterin) (Heparin-binding protein p30).
FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
                                                                          with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material. SIMILARITY: Belongs to the HMGI/HMG2 protein family. SIMILARITY: Concains 2 HMG box DNA-binding domains.
                                                             SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
                                                                                                                                                                                                                                                                                                                                                                                               MGI; MGI:96113; Hmgb1.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; F: cucleus; TAS.

GO; GO:0005615; F: cucleus; TAS.

GO; GO:0006810; F: protein binding; IPI.

GO; GO:0006810; P: pransport; IDA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000135; Highmoblty_2.

Pfam; PF00565; HMG Dox; Z.

PRINTS; PR00886; HIGHMOBLTY12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24763 MW; B3C6A91FD6F1B133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (acidic).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 370; DB 1;
100.0%; Pred. No. 1.7e-31;
Live 0; Mismatches 0;
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E -> V (in Ref. 4)
D -> E (in Ref. 3)
                                                                                                                                                                                                                                           EMBL; Z11997; CAA78042.1; -; mRNA.
EMBL; U00431; AAA20508.1; -; mRNA.
EMBL; L38477; CAA56631.1; -; Genomic_DNA.
EMBL; L38477; AAA57042.1; -; mRNA.
EMBL; BC006586; AA406586.1; -; mRNA.
EMBL; BC083067; AA408565.1; -; mRNA.
EMBL; BC083067; AA483067.1; -; mRNA.
EMBL; BC085090; AA485090.1; -; mRNA.
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HMG box 1.
HMG box 2.
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                                                                                                                                                                                                                                                                                                                                                                  PIR; 148688; 148688.
SNR; P61158; 1-83, 92-170.
MGI: MGI:96113; Hmgbl.
GO: GO:0005615; C:extracellu
GO: GO:0005634; C:nucleus; T:
GO: GO:0005515; F:nitric-oxi
GO: GO:0006809; P:nitric oxi
GO: GO:0006809; P:nitric oxi
GO: GO:0006809; P:nitric oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Conservative
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EKYEKDIAA 160
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DT 01-A
DT 01-A
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DE (Amp
GN Name
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDILINE=91388468; PubMed=1885601;
Medical Sequence J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
Morenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
Merenmies J., Pihlaskari Rauvala H.;
Merenmies J., Partiovarian Jananian and Localization in the Julyopodia of the advancing plasma membrane.";
J. Biol. Chem. 266:16722-16729(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal sequence and production of antipeptide antibodies that detect p30 at the surface of neuroblastoma cells and of brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 34:16596-16607(1995).
-1- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;
MEDLINE-96118376; PubMed=8527432;
Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
Thomas J.O., Laue B.D.;
"Structure of the A-domain of HMG1 and its interaction with DNA as studied by heteronuclear three- and four-dimensional NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93223672; PubMed-8467791;
Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue B.D.,
Thomas J.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure of the HMG box motif in the B-domain of HMG1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the HMG1/HMG2 protein family. SIMILARITY: Contains 2 HMG box DNA-binding domains.
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NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bianchi M.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-88067717; PubMed-3684582;
Paonessa G., Frank R., Cortess R.;
Puoleotide sequence of rat liver HMG1 cDNA.";
Nucleic Acids Res. 15:9077-9077(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;
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O88611_SPAEH PRELIMINARY;
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Best Local Similarity 100.0
Matches 69; Conservative
                                                                                                                                                                                        Q4R844 MACFA PRELIMINARY;
Q4R844;
                                                             Conservative
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                                                    Similarity
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                  Length 214;
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                                                                                                                                                                                                                                                                                                                                                                     24763 MW; B3C6A91FD6F1B133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 370; DB 1;
100.0%; Pred. No. 1.7e-31;
tive 0; Mismatches 0;
                                       PIR; A41175; NSRTH1.
PDB; 1AAB; NNR; @=1-83.
PDB; 1CKT; X-ray; A=7-77.
PDB; 1HMF; NNR; @=88-164.
PDB; 1HMF; NNR; @=88-164.
SMR; P63159; 1-83, 92-170.
Ensembl; ENSRNOG0000030351; Rattus norvegicus.
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Name=HMGB1; ORFNames=RP11-550P23.1-004;
    Y00463; CAA68526.1; -; mRNA.
BC061779; AA461779.1; -; mRNA.
BC081839; AA481839.1; -; mRNA.
BC088402; AA488402.1; -; mRNA.
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                                                                                                                     InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
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QST7C3;
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                                                                                                                                                                                                                                                                                                                                                                      214 AA;
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                                                                                                               2802; Hmgb1
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                    93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152
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                                                                                                                               1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Spalacinae; Nannospalax.
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International consortium for macaque cDNA sequencing, analysis;
"DNA sequences of macaque genes expressed in brain or testis and its
evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                   Gaps
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
box 1 (HMGB1).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
OSada N., Hiratea M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
Substitution rate and structural divergence of 5'UTR evolution:
Comparative analysis between human and cynomolgus monkey cDNAs.";
Subnitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB168615; BAE00728.1; "RNA,
SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;
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Length 215;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
   100.0%; Score 370; DB 2; 100.0%; Pred. No. 1.7e-31;
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088611_SPA
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DT 01-MP
DT 01-MP
DT 01-MP
DE High
GN Name-
OC Bukax
OC Mamma
OC Murid
OC Murid
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61 EKYEKDIAA 69
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Spalacinae; Nannospalax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R HSSP; P07156; INRN.

R GO; GO:0000763; C:chromatin; IEA.

R GO; GO:00005634; C:mucleus; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003675; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000135; Highmoblty_12.

R InterPro; IPR000910; HMG; 12_box.

R PRINTS; PR00886; HIGHWOBLTY12.

R PRINTS; PR00399; HMG; 2.

R RMART; SM0399; HMG; 2.

R PROSITE; PS50118; HMG BOX 2; 2.

C SEQUENCE 215 AA; 24923 MW; 1C6FB6845CAlEGC8 CRC64;
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                                                                                                                                                                                                                  SMR; 088611; 2-84, 93-171.

GO; GO:0000785; C:chrcmatin; IEA.

GO; GO:00005634; C:nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000110; HMG 12_box.

Pfan: PF00505; HMG box: 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                      Lee K.-L.D., Lum H.-K., Nevo E.;
Submitred (AUG-1999) to the EMBL/GenBank/DDBJ databages.
EMBL; AF078B17, AAC27650.2; -; Genomic_DNA.
HSSP; P07156; INHN.
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078818; AAC27651.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTIE; PSS5118; HMG BOX 2; 2. SEQUENCE 215 AA; 24905 MW; 64816B6FCF6033EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 370; DB 2;
100.0%; Pred. No. 1.7e-31;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 370; DB 2; 100.0%; Pred. No. 1.7e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00505; HMG box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High mobility group protein.
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Matches 69, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKYEKDIAA 161
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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088612_SPA
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93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEKKAAKLK 152
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                                                                                                                                                                                                                                                                                                                                                                      Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Spalacinae; Nannospalax.
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Bukaryota, Metazoa, (Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Spalacinae, Nannospalax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee K.-L.D., Lum H.-K., Nevo B.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AROT8819; AAC27652.1; -; Genomic_DNA.
HSSP; P07156; LNHN.
SMR; Q9QWY6; 2-84, 93-171.
SMR; Q9QWY6; 2-84, 93-171.
GO; GO:000785; C:chromatin; IEA.
GO; GO:000785; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:000135; P:Negulation of transcription, DNA-dependent; IEA.
InterPro; IPR000115; Highmobly_12.
InterPro; IPR000910; HMG lox; Z.
Pfam; PF00505; HMG lox; Z.
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO78820; AAC27653.2; -; Genomic_DNA.
HSSP; P07156; 1NHN.
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PROSITE; PS50118; HMG BOX 2; 2.
SROUTENCE 215 AA; 24822 MW; D20D659274B575B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQQX40_SPAEH PRELIMINARY; PRT; 215 AA.
QQX40;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
High mobility group protein.
                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00505; HMG box; 2. PRINTS; PR00886; HIGHMOBLTY12. SMART; SM00398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                   High mobility group protein. Name=HMG1;
                                                                                                                                                       QOWYG SPAEH PRELIMINARY;
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153 EKYEKDIAA 161
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|153 EKYEKDIAA 161
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DR SWR; 090X40; 2-84, 93-171.

DR GO; GO:0000785; C:chromatin; IEA.

DR GO; GO:00005634; C:nucleue; IEA.

DR GO; GO:00005634; F:nucleue; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR000135; Highmoblty_12.

DR Ffam; PF000505; HMG box; 2.

DR FRINTS; PR00886; HIGHMOBLTY12.

DR PROSITE; PS00139; HMG DOX; 2.

DR PROSITE; PS00139; HMG BOX 1; 1.

DR PROSITE; PS0018; HMG BOX 1;
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Search completed: April 6, 2006, 10:25:16 Job time : 82.4836 secs

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Sequence 1, Application US/09214881A
Patent No. 6822078
GRENEAL INFORMATION:
APPLICANT: Carki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Gesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
|||||||||
152 EKYEKDIAA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EKYEKDIAA 69
RESULT 2
US-09-214-881A-1
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LENGTH: 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 883, App
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10813, A
                                                                                                                               (without alignments)
288.890 Million cell updates/sec
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                                                                                                               April 6, 2006, 10:25:39 ; Search time 19.7467 Seconds
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                                                                                                                                                                                                                1 NAPKRPPSAFFLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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US-09-214-881h-1
US-09-214-881h-3
US-09-214-881h-5
US-09-214-881h-5
US-09-214-881h-5
US-09-214-881h-6
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US-09-214-881h-6
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US-09-214-881h-9
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US-09-702-705-705-324
US-09-702-705-705-324
US-09-702-705-7089
US-09-71-128-789
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US-09-614-1248-789
US-09-614-1248-789
US-09-614-1248-789
                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 572060 seqs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                               US-10-717-984-5
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                 Run on:
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Sequence 789, App
Sequence 324, App
Sequence 324, App
Sequence 324, App
Sequence 1667, Ap
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Sequence 10496, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-588-092-883
i Sequence 883, Application US/09538092
i Patent No. 6753314
i GENERAL INFORMATION:
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein Complexes and Method of Using Same FILE REFERENCE: 1596-542
i CURRENT APPLICATION NUMBER: US/09/538,092
i CURRENT FILING DATE: 2000-03-29
i PRIOR APPLICATION NUMBER: 60/127,352
i PRIOR APPLICATION NUMBER: 60/127,352
i PRIOR FILING DATE: 2000-04-01
i NUMBER OF SEQ ID NOS: 1384
i SOFFWARE: CLEAPERSEFFE CONTON NUMBER: 60/178,965
i RIOR FILING DATE: 2000-02-01
i NUMBER OF SEQ ID NOS: 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883
                  US-00-651-563-324

US-09-651-563-324

US-09-519-642-789

US-09-719-642-789

US-09-736-457-1667

US-09-736-457-1667

US-09-674-1248-1667

US-09-678-824-1667

US-09-678-824-1667

US-09-678-824-1667

US-09-678-814-11

US-09-214-881A-11

US-09-214-881A-11

US-09-214-881A-11

US-09-214-964-7

US-09-214-964-7
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Ozaki, Shoichi
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SEQ ID NO 5
LENGTH: 214
TYPE: PRT
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US-09-214-881A-5
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Fatent No. 6822016
Fatent No. 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 214;
                   APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Ogakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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100.0%; Score 370; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0;
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100.0%; Score 370; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0;
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; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
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Nakao, Kazuwa
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152 EKYEKDIAA 160
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152 EKYEKDIAA 160
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// ORGANISM: Homo sapiens

US-09-214-881A-1
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; ORGANISM: Bos taurus
US-09-214-881A-3
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SEQ ID NO 3
LENGTH: 214
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US-09-214-881A-3
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LENGTH: 214
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92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKHPYEKKAAKLK 151
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  GENERAL INFORMATION:

APPLICANT: Sobalima, Junko
APPLICANT: Sobalima, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Ukasuki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitcshi
APPLICANT: Shirakawa, Hitcshi
APPLICANT: Shirakawa, Hitcshi
APPLICANT: Okakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 069383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.6%; Score 365; DB 2; Length 214; Best Local Similarity 98.6%; Pred. No. 1.4e-39; Matches 68; Conservative 0; Mismatches 1; Indels
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APPLICANT: Sobajima, Junko
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Yoshida, Michiteru
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92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151
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APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 069383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
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Pred. No. 3e-34;
4; Mismatches 5; Indel8
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CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SECTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 209
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                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Ozaki, Shoichi
APPLICANT: Usugi, Hiroko
APPLICANT: Usazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
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Best Local Similarity 87.0%;
Matches 60; Conservative
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Best Local Similarity 87.0%;
Matches 60; Conservative
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152 EKYEKDIAA 160
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61 EKYEKDIAA 69
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ORGANISM: Homo sapiens
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US-09-214-881A-6
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                                Sequence 10813, Application US/09949016

Sequence 10813, Application US/09949016

Sequence 1081239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENEUR: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: RestSQ for Windows Version 4.0
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Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same:
FILE REPERENCE: 1596-542
CURRENT APPLICATION NUMBER: US/09/538,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.2%; Score 356; DB 2; Length 213; Best Local Similarity 97.1%; Pred. No. 2.1e-38; Matches 67; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
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PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSedFormatter Version 0.9
LENGTH: 208
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155 EKYEKDIAA 163
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
                           US-09-949-016-10813
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US-09-538-092-1018
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Gaps

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US-09-214-881A-9
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Sequence 10728, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PALING DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 10728
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                        92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151
1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usazaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TILLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 060833.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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87.0%; Pred. No. 3e-34;
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Patent No. 6822078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 EKYEKDIAA 160
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Matches 60; Conserva
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ORGANISM: Human
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LENGTH: 209
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204 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 263
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                                                                                                                                                                                                                                                                                          CIANT: Ozaki, Shoichi

APPLICANT: Sobajina, Junko

APPLICANT: Okazaki, Takahiro

APPLICANT: Okazaki, Takahiro

APPLICANT: Okazaki, Takahiro

APPLICANT: Tanaka, Masao

APPLICANT: Nakao, Katakao

APPLICANT: Shida, Michiteru

APPLICANT: Shida, Michiteru

APPLICANT: Shida, Michiteru

APPLICANT: Osakada, Funio

TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES

FILE REPERENCE: 06838:0104

CURRENT APPLICATION NUMBER: US/09/214,881A

CURRENT FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

LENGTH: 206

TYPE: PPP
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Score 324; DB 2; Length 320;
Pred. No. 5.1e-34;
4; Mismatches 5; Indels
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Sequence 38, Application US/09914259

Sequence 38, Application US/09914259

Patent No. 6495336

GENERAL INFORMATION:

APPLICANT: MYNIAMA, Paul

APPLICANT: Hyman, Paul

TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

FILE REFERENCE: 8471-010-999

CURRENT FILING DATE: 2000-11-21

NUMBER OF SEQ ID NOS: 180

SOFTWARE PRESENCE: Windows Version 4.0

SEQ ID NO 38

LENGTH: 879
  Query Match 87.6%;
Best Local Similarity 87.0%;
Matches 60; Conservative '
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264 EKYEKDIAA 272
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CORGANISM: Homo sapiens
US-09-914-259-38
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Catter, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Pen, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/702,705
NUMBER OF SEQ ID NOS: 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCABAjima, Junko
APPLICANT: Obasjima, Junko
APPLICANT: Obaszaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
FILE REPERENCE: 098383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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Query Match 85.7%; Score 317; DB 2; Length 879; Best Local Similarity 88.4%; Pred. No. 1.5e-32; Matches 61; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 81.1%; Score 300; DB 2; Length 201; 1 Similarity 79.4%; Pred. No. 3.9e-31; 54; Conservative 6; Mismatches 8; Indels
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US-09-702-705-324
Sequence 324, Application US/09702705
Parent No. 6504010
GENERAL INFORMATION:
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APPLICANT: Ozaki, Shoichi
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827 EKYKKDIAA 835
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ORGANISM: Gallus gallus
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150 EKYEKDVA 157
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Best Local Similarity
Matches 54; Conserva'
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US-09-214-881A-10
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; SEQ ID NO 324
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-324

Query Match

Query Match

Best Local Similarity 79.4%; Pred. No. 2.4e-30;

Matches 54; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 60

Qy 1 NAPKRPPSGFFLFCSEFRENKIKSTNPGISIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 150

Qy 61 EKYEKDIA 68

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Db 151 EKYEKDVA 158

Search completed: April 6, 2006, 10:27:52
Job time: 19.7467 secs
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Query Match
Best Local Similarity
Matches 69; Conserv
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Sequence 51, Appl
Sequence 51, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 68, Appl
Sequence 58, Appl
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439.516 Million cell updates/sec
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                                                             April 6, 2006, 10:26:34 ; Search time 65.5954 Seconds
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Sequence
Sequence
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1 NAPKRPPSAFFLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA
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/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-300-072-5
US-10-456-949-5
US-10-456-949-5
US-10-718-495-5
US-10-718-495-5
US-10-718-495-5
US-10-718-945-5
US-10-718-945-5
US-10-938-992-67
US-10-938-992-76
US-10-938-992-76
US-10-938-992-76
US-10-938-992-76
US-10-938-992-76
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US-10-938-992-73
US-10-938-92-348
US-10-938-92-36
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US-10-087-192-1446
US-10-147-447-1
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                                                                                                                                                                                                                                                                Published Applications AA Main:*
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Listing first 45 summaries
                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                     Sequence 2
Sequence 1
Sequence 2
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Sequence 1
Sequence 4
Sequence
Sequence
Sequence
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US-10-300-072-5
5 Sequence 5, Application US/10300072
5 Publication No. US20030144201A1
5 GENERAL INFORMATION:
5 APPLICANT: Kevin J. Tracey
7 APPLICANT: Howland Shaw Warren, Jr.
7 APPLICANT: Mitchell P. Fink
7 TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
7 TITLE OF INVENTION: AGENTS
7 TITLE OF INVENTION: AGENTS
7 FILE REFERENCE: 3268.1001-005
7 CURRENT APPLICATION NUMBER: US/10/300,072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 370; DB 4; Length 69; 100.0%; Pred. No. 5.5e-37; ive 0; Mismatches 0; Indels
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US-10-147-447-5

Sequence 5, Application US/1014747

Publication No. US20030060410A1

GENERAL INFORMATION:

APPLICANT: Yarag, Huan

APPLICANT: Warren Jr., Howland Shaw

APPLICANT: Warren Jr., Howland Shaw

TITLE OF INVENTION: Ant.-Inflammatory Agents

TITLE OF INVENTION: Ant.-Inflammatory Agents

CURRENT APPLICATION NUMBER: US/10/147,447

CURRENT APPLICATION NUMBER: 60/291,034

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR PRING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEG for Windows Version 4.0

SEQ ID NO 5

LENGTH: 69
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US-10-938-992-74
US-10-087-192-1443
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US-10-868-577A-63
US-10-868-549-22
US-10-938-992-18
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US-10-718-495-2
US-10-717-984-1
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ORGANISM: Homo sapiens
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FILE REFERENCE: 3268.1001-007
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Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Huan Yang

TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

FITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
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                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                 ch 100.0%; Score 370; DB 4; 1 Similarity 100.0%; Pred. No. 5.5e-37; 69; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Huan Yang
TITLE OF INVENTION: USE OF HMG FRAGWENTS AS
TITLE OF INVENTION: USE OF HMG FRAGWENTS AS
TITLE OF INVENTION: USE OF HMG FRAGWENTS
FILE REFERENCE: 3268.1001.006
CURRENT FILING DATE: 2003.06-06
PRIOR FILING DATE: 2003.06-06
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2001-05-15
SEQ ID NOS: 23
SOFTWARE: FASEESEQ for Windows Version 4.0
            PRIOR APPLICATION NUMBER: US 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 69
TYPE: PRT
ORGANISM: Homo sapiens
2002-11-20
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Best Local Similarity
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Matches 69; Conserva
CURRENT FILING DATE:
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US-10-456-949-5
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US-10-456-947-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 370; DB 4;
Pred. No. 5.5e-37;
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; Sequence 5, Application US/10717984
; Sequence 5, Application No. US20040156851A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
; FILE REFERENCE: 3258.1008-001
; CURRENT APPLICATION NUMBER: US/10/717,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
CURRENT APPLICATION NUMBER: US/10/456,947
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Mouse/ rat/ human US-10-456-947-5
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Best Local Similarity 100.0%;
Matches 69; Conservative 0
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us-10-717-984-5.rapbm

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FILE REFERENCE: 3268.1001-007
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
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CORGANISM: Homo sapiens
US-10-718-495-51
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nes 69; Conserv
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Matches
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Publication No. US20040053841A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/10300072

Sequence 51, Application US/10300072

Publication No. US2030144201A1

GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
APPLICANT: Huan Yang
APPLICANT: Huan Yang
APPLICANT: Mitchell P. Fink
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLANMATORY
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLANMATORY
TITLE OF INVENTION: USE OF HMGB FRAGMENTS
CURRENT FILING DATE: 2002-11-20
FRIOR APPLICATION NUMBER: US 10/147,447
FRIOR APPLICATION NUMBER: US 60/291,034
FRIOR APPLICATION NUMBER: US 60/291,034
FRIOR APPLICATION NUMBER: US 60/291,034
SEQ ID NO 51
LENGTH: 74
LENGTH: 74
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,846
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 69
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61 EKYEKDIAA 69
                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-10-300-072-51
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US-10-300-072-51
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US-10-456-947-37
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                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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US-10-718-495-51

Sequence 51, Application US/10718495

Publication No. US20040141948A1

GENERAL INPORMATION:

TITLE OF INVENTION: USE OF HMGB FRACMENTS AS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

CURRENT APPLICATION NUMBER: US/10/718,495

CURRENT FILING DATE: 2003-11-12

PRIOR PAPLICATION NUMBER: 60/427,841

PRIOR PILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FARSEQ for Windows Version 4.0

SEQ ID NO 51

LENGTH: 74
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TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
FILE REFERENCE: 3298.1008-001
CURRENT APPLICATION 12, 10/10/717, 984
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427, 846
CURRENT APPLICATION NUMBER: US/10/456,947
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR PRILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-938-992-76
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                                                                                                                                                                                           100.0%; Score 370; DB 4; Length 74; 100.0%; Pred. No. 6e-37; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/10938992
| Sequence 67, Application US/10938992
| Publication No. US20050152903A1
| GENERAL INFORMATION:
| APPLICANT: Newman, Walter
| APPLICANT: Oin, Shixin
| APPLICANT: Oin, Shixin
| APPLICANT: Obst. Robert
| TITLE OF INVENTION: Wonoclonal Antibodies Against HMGB1
| TITLE OF INVENTION: WONOCLONAL ANTIBODIES AGAINST HMGB1
| FILE REFERENCE: 3258.1033-001
| CURRENT APPLICATION NUMBER: US/10/938,992
| CURRENT APPLICATION NUMBER: 60/502,568
| PRIOR PILING DATE: 2003-09-11
| NUMBER OF SEQ ID NOS: 76
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 74
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APPLICANT: O'Reefe, Theresa
APPLICANT: O'Reefe, Theresa
APPLICANT: O'Reefe, Theresa
TILE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REPERENCE: 3258.1033-001
CURRENT APPLICATION NUMBER: US/10/938,992
CURRENT FILING DATE: 2004-09-10
PRIOR PRIOR APPLICATION NUMBER: 60/502,568
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                 NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 74
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US-10-938-992-76
Sequence 76, Application US/10938992
Publication No. US20050152903A1
GENERAL INFORMATION:
APPLICANT: Newman, Walter
PRIOR FILING DATE: 2002-11-20
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Best Local Similarity 100.
Matches 69; Conservative
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                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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EKYEKDIAA 73
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Best Local Similarity
Matches 69; Conserval
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US-10-938-992-67
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Publication No. US20040053841A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
TITLE OF INVENTION: HAGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REPERENCE: 3268.1001-007
CURRENT APPLICATION NUMBER: US/10/456,947
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GRUERAL INFORMATION:
APPLICANT: Han Yang
APPLICANT: Howland Shaw Warren, Jr.
APPLICANT: Howland Shaw Warren, Jr.
APPLICANT: Mitchell P. FWA
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
FILE REPRENCE: 3268.1001-005
CURRENT APPLICATION NUMBER: US/10/300,072
CURRENT FILING DATE: 2002-11-20
FRIOR APPLICATION NUMBER: US/10/47,447
FRIOR FILING DATE: 2002-05-15
FRIOR APPLICATION NUMBER: US 60/291,034
FRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFWWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 92
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100.0%; Score 370; DB 5;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 69; Conservative 0; Mismatches 0
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 74
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Publication No. US20030144201A1
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Best Local Similarity 100.0
Matches 69; Conservative
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1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNVTAADDKQPYEKKAAKLK 60
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US-10-718-495-58
Sequence 58, Application US/10718495
Publication No. US20040141948A1
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF HWGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
CURRENT APPLICATION NUMBER: 2003-11-12
PRIOR FILING DATE: 2003-11-12
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 92
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR RILING DATE: 2001-05-15
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 92
; TYPE: PRT
; ORGANISM: HOMO Sapiens
US-10-456-947-43
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; ORGANISM: Homo sapiens
US-10-718-495-58
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65 EKYEKDIAA 73
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Search completed: April 6, 2006, 10:32:47 Job time : 66.5954 secs

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Sequence 1443, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Van
APPLICANT: AAdarmani, Susan
APPLICANT: Tang, Y. Tom
TILLE OF INVENTION Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
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ORGANISM: Homo sapiens
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Sequence 11, Appl
Sequence 12, Appl
Sequence 122, Appl
Sequence 26884, Ap
Sequence 26884, Ap
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Sequence 1364, Ap
Sequence 2564, Ap
Sequence 1066, Ap
Sequence 9680, Ap
Sequence 32735, A
Sequence 32734, A
Sequence 32734, A
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1: /SIDS5/ptodata/2/pubpaa/US06_NEW PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US07_NEW PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW PUB.pep:*
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5: /SIDS5/ptodata/2/pubpaa/US07_NEW PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-10-821-234-1443
US-11-186-422-11
US-11-186-422-12
US-11-169-041-192
US-11-096-568A-26883
US-11-096-568A-26883
US-11-087-099-8038
US-11-087-099-9518
US-11-087-099-9518
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US-11-087-099-9518
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Maximum Match 100%
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                  US-11-096-568A-15614
US-11-096-568A-15614
US-11-096-568A-15614
US-11-087-099-7075
US-11-087-099-7075
US-11-172-740-1565
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US-11-172-740-1572
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US-11-124-368A-309
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US-11-172-740-1570
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Publication No. US20060057679A1

GENERAL INFORMATION:

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: O'Keefe, Theresa

CURRENT APPLICATION NUMBER: US/11/186,422

CURRENT APPLICATION NUMBER: 06/589,678

PRIOR FILING DATE: 2004-07-20

RIOR APPLICANION NUMBER: 60/589,678

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
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Matches 69; Conservative
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                                                                                                                                                                                                                                                    Length 215;
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Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0;
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US-11-15

Sequence 11, Application US/11186422

Publication No. US20060057679A1

GENERAL INPORMATION:

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: O'Keefe, Theresa

APPLICANT: O'Keefe, Theresa

APPLICANT: Oin, Shixin

TILE OF INVENTION: RAGE PROTEIN DERIVATIVES

FILE REPERENCE: 3.258.1021-003

CURRENT APPLICATION NUMBER: US/11/186,422

CURRENT FILING DATE: 2.005-07-20

PRIOR APPLICATION NUMBER: 60/589,678

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 11
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; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION: Therapeutics, Inc.
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: Usciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RASE PROTEIN DERIVATIVES
; TITLE REFERENCE: 3258-1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
CURRENT FILING DATE: 2004-04-07
PRIOR PEDLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SEQ TWARE: DL SEQ_genes Version 1.0
SEQ ID NO 1443
LENGTH: 215
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                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443
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TYPE: PRT
CRGANISM: Homo sapiens
US-11-186-422-11
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Best Local Similarity
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Application: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: True OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT PAPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
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Best Local Similarity 88.4%; Pred. No. 7.4e-30;
Matches 61; Conservative 1; Mismatches 7;
                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 215
TYPE: PRT
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|53 EKYEKDIAA 161
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                                                                                                                               ORGANISM: Mus musculus US-11-186-422-12
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CRGANISM: Homo sapiens
US-11-169-041-192
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44.6%; Score 165; DB 7; Length 92;
Best Local Similarity 47.1%; Pred. No. 8e-13;
Matches 32; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8838, Application US/11087099; Sequence 8838, Application US/20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(51450) B EP; CURRENT APPLICATION UNMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 8838
LENGTH: 92
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Publication No. US20060041961A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FIRE REPERENCE: 38-21(53450) B P
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3073
                                                                                                                                                                                                                 Query Match 45.5%; Score 168.5; DB 7; Best Local Similarity 48.4%; Pred. No. 7.1e-13; Matches 31; Conservative 13; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
44.5%; Score 164.5; DB 7;
Best Local Similarity 47.1%; Pred. No. 1.5e-12;
Matches 33; Conservative 12; Mismatches 24;
                                    TYPE: PRT
ORCANISM: Zea mays subsp. mays
FEATURE:
LOCATION: (1). (187)
OTHER INFORMATION: Ceres Seq. ID no. 13627625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Canavalia gladiata
US-11-087-099-3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EKYEKDIA 68
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77 KRYEKEKA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                              142 DYEK 145
                                                                                                                                                                                                                                                                                                                                                                                                  62 KYEK 65
                                                                                                                                                                            US-11-096-568A-26883
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US-11-087-099-8838
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US-11-087-099-3073
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SEQ ID NO 26883
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Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Therby

FILE REPRENCE: 2750-1592PUS2

CURRENT APPLICATION WHMBER: US/11/096,568A

CURRENT APPLICATION WHMBER: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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                                                                                                                                                                                                                                                                                                                                 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.5%; Score 168.5; DB 7;
48.4%; Pred. No. 5e-13;
tive 13; Mismatches 19;
                                                                                                                                                                                              i LOCATION: (1)...(169)
i OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234
                                                                                                                                                                                                                                                                                   Score 279; DB 6;
Pred. No. 3.7e-26;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , LOCATION: (1).7(139)
, OTHER INFORMATION: Ceres Seq. ID no. 13627626
US-11-096-568A-26884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26884, Application US/11096568A, Publication No. US20060048240A1, GENERAL INFORMATION:
                    NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1234
LENGTH: 169
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays subsp. mays
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Best Local Similarity 75.0%;
Matches 51; Conservative
PRIOR FILING DATE: 2003-04-07
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Matches 31; Conservative
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140 EEYGKDFA 147
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US-11-096-568A-26883
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US-11-096-568A-26884
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SEQ ID NO 3510
LENGTH: 149
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  1 NAPKRPPSAFFLFCSEYRPKIKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKL 59
                      1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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US-11-087-099-9518
i Sequence 9518, Application US/11087099
i Publication No. US20060041961A1
i GENERAL INFORMATION:
i APPLICANT: Abad, Mark S. et al.
i TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
i CURRENT FILING DATE: 2005-03-22
i NUMBER OF SEQ ID NOS: 12464
i SEQ ID NO 9518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 44.1%; Score 163; DB 7; Length 93; Best Local Similarity 45.5%; Pred. No. 1.4e-12; Matches 30; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                          US-11-087-099-869
Sequence 869, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TILLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 869
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CTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-9518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-087-099-869
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KEEYDKSILA 104
                                                                                    KEKYEKDIAA 69
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KRYESE 84
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79 KRYESE 84
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Sequence 1571, Application US/11172740
; Publication No. US2006005724A1
; Sequence 1571, Application US/11172740
; Publication No. US2006005724A1
; GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: UNCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR N
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; CURRENT APPLICATION NUMBER: US/11/72,740
; CURRENT APPLICATION NUMBER: 60/583,621
PRIOR FILING DATE: 2004-06-30
; RIOR PILING DATE: 2004-06-30
; RIOR PILING DATE: 2004-06-30
; RIOR PILING DATE: 2004-06-30
; RIOR FILING DATE: 2004-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: Utility: Useful for making ornamental plants with modified flowers
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          Sequence 3510, Application US/11087099
Publication No. US20060041961A1
Publication INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT FILIAND NUMBER: US/11/087,099
CURRENT FILIAND DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
43.9%; Score 162.5; DB 7;
Best Local Similarity 44.3%; Pred. No. 2.8e-12;
Matches 31; Conservative 14; Mismatches 24;
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NAME/KY: misc feature
LOCATION: (1) [149)
OTHER INFORMATION: Public GI no. 729737
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NAME/KEY: misc_feature
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-087-099-3510
US-11-087-099-3510
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US-11-172-740-1571
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LOCATION:
OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
                                                                                  ; OTHER INFORMATION: Utility: Useful for making plants with increased biomass US-11-172-740-1571
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                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                            Query Match 43.9%; Score 162.5; DB 7; Length 149; Best Local Similarity 44.3%; Pred. No. 2.8e-12; Matches 31; Conservative 14; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.1%; Score 159.5; DB 7; Length 141; Best Local Similarity 44.3%; Pred. No. 6.1e-12; Matches 31; Conservative 13; Mismatches 25; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9185, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
GAPELICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450) B BP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT APPLICATION NUMBER: US/11/087,099
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9185
; LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 6, 2006, 10:33:31
Job time : 9.625 secs
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103 KEEYEITLQA 112
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94 KAEYQKNMDA 103
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                                           FEATURE:
NAME/KEY: misc_feature
LOCATION:
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US-11-087-099-9185
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6, 2006, 10:12:19 ; Search time 24.2763 Seconds (without alignments) 361.981 Million cell updates/sec
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                         2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                  protein search, using sw model
                                                                                                                                          110
1 FKDPNAPKRLPSAFFLFCSE 20
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

	Description	Aae35864 Human HMG	Ado25940 Tumour ne		Aae35868 Human HMG	Ado25937 Human hig	Ado25958 High mobi	Ado71496 Human hig	Ado71529 Human hig	Human	Ady85333 High mobi	_	•	Human	Ado25936 Human hig	Ado71495 Human hig	Human	Adp30030 Human sec	Aae35866 Human HMG	Ado25935 Wild type	Ado25941 Human HMG	Ado71494 Human hig	Ado71500 Human hig	Ady85335 High mobi	Ady85331 Human hig
SUMMARIES	OI.	AAE35864	AD025940	AD071499	AAE35868	AD025937	AD025958	AD071496	AD071529	ADY85364	ADY85333	ADY85080	ADY85014	AAE35867	AD025936	AD071495	ADY85379	ADP30030	AAE35866	AD025935	AD025941	ADO71494	ADO71500	ADY85335	ADY85331
	DB	9	ω	œ	9	œ	œ	ω	æ	6	σ	σ	σ	9	8	œ	σ	œ	9	8	œ	æ	æ	0	0
	Length	20	20	20	74	74	74	74	74	74	74	74	74	182	182	182	182	213	216	216	216	216	216	216	216
•	* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110
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Human High High	Ado25934 High mobi Ado71530 Human hig Ado71527 Human hig	Ady85367 Human hig Ady85367 Human hig Ady85362 Human hig Ady85365 Human hig		Ady85087 Human HMG Ado25962 High mobi Ado71534 Human hig	Ady85084 Human HMG Ady85084 Human HMG Aab53515 Human col Aab57179 Human pro Aag75983 Human col
ADY85012 ADO25961 ADO25959	AD025934 AD071530 AD071527	ADY85367 ADY85362 ADY85365	ADY85083 ADY85078 ADY85081	ADY85087 ADO25962 ADO71534	ADY85084 AAB53515 AAB57179 AAG75983
216 9 74 8 74 8	8 8 8 8 0	44.4	444	4 2 2 2 6	92 92 121 128 128 4
100.0 93.6 93.6	93.0 93.0	9999	, 60 60 60 60 60 60 60 60	93.6	
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25 26 27	8 6 0 F	1 W W W	3 9 9 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	8 6 6 4 4	. 4. 4. 4. 4. 4. 6. 4. 7.

ALIGNMENTS

inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis; apparial ulcer; duodenal ulcer; Crohn's disease; meningitis; allergy; immune complex disease; sinusitis; bronchitis; atherocelerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; amochiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene therapy; human immunodeficiency virus; HMGB1 protein. Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma; AAE35864 standard; peptide; 20 AA. Human HMG1 B box fragment #1. (first entry) Homo sapiens. 17-JUN-2003 AAE35864; AAE35864

WO200292004-A2.

21-NOV-2002.

15-MAY-2002; 2002WO-US015329.

15-MAY-2001; 2001US-0291034P.

(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. (GEHO) GEN HOSPITAL CORP. (UYPI-) UNIV PITISBURGH.

WPI; 2003-120594/11.

MP; Fink

Yang H, Warren HS,

Tracey KJ,

New isolated polypeptide having a vertebrate HMG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.

Example 4; Page 45; 82pp; English.

The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-

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                         cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's disease, peritonitis, heparitis, asthma, allergy, immune complex disease, sinusitis, bronchitis, emphysema, HV infection, candidiasis, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, meningitis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMGI (also termed as HMGBI) B box
naturally occurring HMG A box inhibits the release of a pro-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine; pharmaceutical composition; HMGB B box, high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity; INF stimulating; tumour necrosis factor stimulating.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 110; DB 6; 100.0%; Pred. No. 2.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                          fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ID AD02

XX AD02

XX AD02

XX AD02

XX HWGB

KW HWGB

KW COYLO

KW COWLO

KW COWLO

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immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of tumour necrosis factor

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The invention relates to a polypeptide comprising a high mobility group box procein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that considering along the HMGB box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an a patient comprises administering to the patient an amount of the collypeptide. The polypeptide. The ploopistion and methods are cuseful in treating obesity and conditions characterised by activation of an oplypeptide. The polypeptide characterised by activation of an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; high mobility group box 1 B box; HMGB1 B box; HMGB; HMGB A box; hmMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; peritonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human high mobility group box 1 (HMGB1) B box protein active fragment #2.
(TNF) stimulating peptide based on amino acids 1-20 of the human high mobility group box 1 (HMG1) protein.
                                                                                                                                            Gaps
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                                                                                                     Length 20;
                                                                                                                                        Indels
                                                                                                Score 110; DB 8;
Pred. No. 2.5e-09;
                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 33; SEQ ID NO 23; 113pp; English.
                                                                                                                                                                                                                                                                                                                     AD071499 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                               1 FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                        1 FKDPNAPKRLPSAFFLFCSE
                                                                                                     100.08;
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20-NOV-2002; 2002US-0427846P.
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                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                 Local Similarity 100.
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                                                           Sequence 20 AA;
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                                                                                                     Query Match
                                                                                                                                          Matches
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ADO71499
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disease, peritonitis, hepatitis, asthma, allergy, immune complex disease

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           chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcer, 8 disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB1 B box polypeptide active fragment of the
rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis; appendicitis; peptic ulcer; duodenal ulcer; crohn's disease; meningitis; allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer; a disease; Goodpasture's syndrome; graff-versus-host disease; amoebiasis; multiple sclerosis; gout; cerebral infarction; peritohitis; gene therapy; human immunodeficiency virus; HMGBI protein; mutant;
                                                                                                                                                                                            Gaps
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                                                                                                                                                          Length 20;
                                                                                                                                                          100.0%; Score 110; DB 8; Length 2
100.0%; Pred. No. 2.5e-09;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                          AAE35868 standard; protein; 74 AA
                                                                                                                                                                                                                                              FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                                           FKDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human HMG1 protein mutant #2.
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                                                                                                                                                                                             20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120594/11
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                             Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200292004-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
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                                                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                            AAE35868;
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                                                                                                                                                                                                                                                                                                            RESULT
8888888888888
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The invention relates to high mobility group (HMG) protein comprising DNA binding motifs tremed HMG A box and HMG B box. HMG A box or a non-naturally occurring HMG A box inhibites the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's

Example 1; Page 37; 82pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual. This is the amino acid sequence of a human high mobility group box 1 (HMG1) B box mutant.
           sinustiis, bronchitis, emphysema, HIV infection, candidasis, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMGI (also termed as HMGBI)
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; gene therapy; vaccine; pharmaceutical composition;
HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity;
                                                                                                                                                                                                                                ö
                                                                                                                                                                                           Length 74;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                             100.0%; Score 110; DB 6; 100.0%; Pred. No. 8.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human high mobility group box 1 B-box mutant.
                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                   1 FKDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                                                                                                                                                                                                                             AD025937 standard; protein; 74
                                                                                                                                                                                                                                                                                         FKDPNAPKRLPSAFFLFCSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                             Local Similarity 100.
les 20; Conservative
                                                                                                                      protein (B box) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-420625/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004046338-A2
                                                                                                                                                           Seguence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2004
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                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                 Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                          RESULT 5
AD025937
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Human high mobility group box 1 (HMGB1) mutant protein #2.

(first entry)

26-AUG-2004

ADO71496;

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Human; high mobility group box 1, HMGB1, HMGB, HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; asthms; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; reperfusion ischaemia; Behcet's disease; organic ischaemia; reperfusion ischaemia; Behcet's disease; gratt-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-420628/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pharmaceutical composition comprises a polypeptide comprising an HMGB B box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.
                                                                                                                                                                                                                                                                                      cytostatic; gene therapy, vaccine; pharmaceutical composition;
HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant, stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMG1) B box biologically active fragment.
                                     Gaps
                                     ö
       Length 74;
                                  Indels
                                                                                                                                                                                                                                                          High mobility group box 1 B box fragment seqid 41.
   100.0%; Score 110; DB 8;
100.0%; Pred. No. 8.9e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 110; DB 8;
100.0%; Pred. No. 8.9e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 41; 68pp; English.
                                                                                                                                                                   ADO25958 standard; peptide; 74 AA
                                                               FKDPNAPKRLPSAFFLFCSE 20
                                                                              19-NOV-2003; 2003WO-US036975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2002; 2002US-0427848P
                                                                                                                                                                                                                                (first entry)
Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-420625/39.
                                                                                                                                                                                                                                                                                                                                                                                 WO2004046338-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                              26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracey KJ;
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                                                                                                                                                                                                  AD025958;
                                                                                                                                      RESULT 6
ADO25958
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(CRIT-) CRITICAL THERAPEUTICS INC.

Newman W, O'keefe TL;

20-NOV-2003; 2003WO-US037507. 20-NOV-2002; 2002US-0427841P. 20-NOV-2002; 2002US-0427846P

WO2004046345-A2.

Synthetic.

Ношо

03-JUN-2004

mutant; mutein sapiens.

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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinfilammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinfilammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obsesty in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMP biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obseity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obseity and conditions characterised by activation of a polypeptide. The polypeptides antibodies, composition and methods are useful in treating obseity and conditions characterised by activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an inflammatory cytokine cascade, e.g. sepais, allograft rejection, rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, mycardial ischaemia, organic ischaemia, reperfusion ischaemia, abecet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB1 mutant polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 110; DB 8;
100.0%; Pred. No. 8.9e-09;
ive 0; Mismatches 0;
Example 1; SEQ ID NO 20; 113pp; English.
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nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 74 AA;
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Matches
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Gaps

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Indels

100.08; PAN 100.08; PAN

20; Conservative

Matches

Local Similarity

Query Match

20

1 FKDPNAPKRLPSAFFLFCSE 20

1 FKDPNAPKRLPSAFFLFCSE

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ADO71496 standard; protein; 74 AA.

RESULT 7 ADO71496 ID ADO7 XX

Length 74;

1 FKDPNAPKRLPSAFFLFCSE 20

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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B confitoring weight loss or treating obesity in a patient, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMP biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine caccade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an another activation of an activation of an activation and methods are useful in treating obesity and conditions characterised by activation of an activation of an activation and methods are useful an amount of the patient an amount of the patient and activation of an activation of an activation of an activation and methods are activation of an a
                                                                                                                                                                                                                                                                                                Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; finflammatory cytokine cascade; sepsis; allogaft rejection; rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; peritonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; aultiple sclerosis; cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB B box polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
                                                                                                                                                                                                                                                  Human high mobility group box (HMGB) B box protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 53; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CRIT-) CRITICAL THERAPEUTICS INC
                                                          ADO71529 standard; protein; 74 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2002; 2002US-0427841P.
20-NOV-2002; 2002US-0427846P.
                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                     26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-2004.
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                                                                                                                          AD071529;
RESULT 8
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The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has been the antibody response to the administered antigen. HMGB1 polypeptide comprising a vertebrate the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immune puppressive fragment of the vertebrate or non-natural HMGB A box. The immune comprises administering the administration of a non-human antigen, non-adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of individual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune pathology, inhibiting an immune pathology, inhibiting an immune pathology, inhibiting an individual or decreasing an immune response to an administered non-human antigen comprise administering a Wertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural A box.

Comprises administering a HMGB polypeptide comprising a vertebrate HMGB A comprises administering an attoimmune disease is allergy, comprise and a vertebrate or non-naturally-occurring HMGB B cox. The HMGB polypeptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, uncertaint a the C-terminus. The autoimmune disease is allergy, uncertaint a disease, asthem, rheumatoid arthritis, culorasis or systemic lupus erythemates uncertaint of the B box of human HMGILIO, a HMGB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its
                                                                                                                                                                                                                                                                                                                   High mobility group box; HWG1L10; immune disorder; infection; immunosuppressive; autoimmune disease; allergy; antiallergic; ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiasthmatic; rheumatoid arthritis; antitheumatic; antiarthritit; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
                                                                                                                                                                                                                                                                          Human high mobility group box protein HMG1L10 B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 39; 57pp; English.
                                                                                                                                   ADY85364 standard; protein; 74 AA
FKDPNAPKRLPSAFFLFCSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2004; 2004WO-US029540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2003; 2003US-0502349P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive fragment.
                                                                                                                                                                                                                              02-JUN-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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                                                                                                                ADY85364
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Gaps

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100.0%; Score 110; DB 8; Length 74; 100.0%; Pred. No. 8.9e-09; tive 0; Mismatches 0; Indels

20; Conservative

Best Local Similarity Matches 20, Conserv

Query Match

Sequence 74 AA;

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; autoimmune disconse, allergy; antiallergic; ulcerative colitis; autoimmune allergy; antiallergic; ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiasthmatic; rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer; mutein.
                                                                                                                                                    Gaps
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                                                                                                                                                    ;
0
                                                                                          Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High mobility group box; HMGB1; immune disorder; infection;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High mobility group box protein HMGB1 B box mutant.
                                                                                                                                                    0
                                                                                   100.0%; Score 110; DB 9;
100.0%; Pred. No. 8.9e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ADY85333 standard; protein; 74 AA
                                                                                                                                                                                                                                                       FKDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                                             1 FKDPNAPKRLPSAFFLFCSE 20
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                                             Query Match
Best Local Similarity
'... 20; Conservative
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                         Sequence 74 AA;
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Rattus sp.
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A claimed method of treating an autoimmune disorder in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box, or an immunosuppressive
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or an immunosuppressive fragment of the vertebrate or non-natural A box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                  fragment of these, and a vertebrate or non-naturally-occurring HMGB B box. The HMGB polypoptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, psoriasis or systemic lupus erythematosus (all claimed). The present sequence is that of a mutated B box of human, mouse and rat HMGBI proteins ADY85326-ADY85327, which was produced in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High mobility group box; HMGB1; monoclonal antibody; antibody therapy, sepsis, antiboacterial immunosuppressive; graff rejection; arthritis; antiarthritic; asthmatic; lupus erythematosus; antiarthritic; asthmation; dermatological; respiratory distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress; parchice obstructive pulmonary disease; pancratis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; asstrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                     Length 74;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 110; DB 9;
100.0%; Pred. No. 8.9e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2; 123pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADY85080 standard; protein; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                        1 FKDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-233483/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HMGB1 A box.
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                                                                                                                                                                                                                                                                                          Sequence 74 AA;
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                                                                                                                                                                                                                                              invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADY85080;
                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB colypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine caseade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB hox but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB correction. A method of treating a condition characterized by activation of an inflammatory cytokine caseade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult crespiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1. An identical

invention provides antibodies, or their antigen-binding fragments,

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polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody for antigenbinding fragment) binds to a vertebrate HMGB, and inhibits release of specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB protein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High mobility group box; HMGB1; monoclonal antibody; antibody therapy; sepsis, antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiarthmatic; lupus erythematosus; antiarthation; dermatological; respiratory; inflammation; dermatological; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritoritis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
                                                                                                                                                                                                                                                     and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1 ADY85012. An identical sequence is also found in rat and mouse HMGB1.
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 110; DB 9; Length 74; 100.0%; Pred. No. 8.9e-09; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
ses 20; Conservative
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                                                                                                                                                                                                                                                                                                                                     Sequence 74 AA;
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Gapa

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Length 74; Indels

100.0%; Score 110; DB 9; 100.0%; Pred. No. 8.9e-09;

Sequence 74 AA;

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Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis; appendicitis; peptic ulcer; duodenal ulcer; crohn's disease; meningitis; allery; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease; amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene, therapy; human immunodeficiency virus; HMGBI protein; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polypeptide having a vertebrate HMG A box, useful for
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. (GEHO ) GEN HOSPITAL CORP. (UYPI-) UNIV PITTSBURGH.
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                                                                                                                                                                               AAE35867 standard; protein; 182 AA
                                                                                       1 FKDPNAPKRLPSAFFLFCSE 20
                                                                      1 FKDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang H, Warren HS,
                                                                                                                                                                                                                                                                        Human HMG1 protein mutant #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2002; 2002WO-US015329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2001; 2001US-0291034P
Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                        17-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tracey KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                  RESULT 13
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New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful for treating, e.g. sepsis.

Newman W, Qin S, Okeefe T, Obar R; (CRIT-) CRITICAL THERAPEUTICS INC.

WPI; 2005-233483/24.

11-SEP-2003; 2003US-0502568P.

Disclosure; SEQ ID NO 2; 123pp; English.

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The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-naturally occurring HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatory cytokine cascade such as endotoxic shock, rheumatorid arthritis, appendictis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, asthma, allergy, immune complex disease, sinusitis, bronchitis, emphysema, HIV infection, candidasis, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, dermatitis, and prosential infarction, neuritis, Goodpasture's syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMG1 (also termed as HMGB1)
   cytokine
inhibiting a condition associated with an activated inflammatory cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.
                                                                                                                 Example 1; Page 37; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy. The present sequence is 
protein (carboxy terminus) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 182 AA;
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100.0%; Score 110; DB 6; 100.0%; Pred. No. 2.1e-08; ö 20; Conservative Local Similarity Query Match Matches

Mismatches

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Gaps

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Length 182; Indels

> 1 FKDPNAPKRLPSAFFLFCSE 20 89 욥 ò

AD025936 standard; protein; 182 AA AD025936; RESULT 14 AD02593

(first entry) 26-AUG-2004

Human high mobility group box 1 C-terminal mutant.

cytostatic; gene therapy, vaccine; pharmaceutical composition; HMGB B box; high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity; mutant; mutein.

Homo sapiens.

Synthetic.

WO2004046338-A2

03-JUN-2004

20-NOV-2002; 2002US-0427848P

19-NOV-2003; 2003WO-US036975

(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.

Tracey KJ

WPI; 2004-420625/39

New pharmaceutical composition comprises a polypeptide comprising an HMGB box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.

Example 1; SEQ ID NO 19; 68pp; English.

The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for

The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                        immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of a human high mobility group box 1 (HMG1) C-terminal mutant.
functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HWGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                               ; Score 110; DB 8;
; Pred. No. 2.1e-08;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 FKDPNAPKRLPSAFFLFCSE 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO71495 standard; protein; 182
                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Query Match
Best Local Similarity 100.0.
Cheq 20; Conservative
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                                                                                                                                                                                                                                                                                                                           Sequence 182 AA;
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CC detecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HWGB protein or an antibody that binds to the protein, an agent that inhibits TNF biological activity and a method of treating a condition in a patient characterised by activation of an conflammatory cytokine cascade. Effecting weight loss or treating obesity of in a patient comprises administering to the patient an amount of the colypeptide. The polypeptide, antibodies, composition and methods are conseful in treating obesity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, can inflammatory cytokine cascade, e.g. sepsis, allograft rejection, controucive pulmonary disease, psoriasis, pancreating, crownic obstructive pulmonary disease, psoriasis, pancreating, contronic obstructive a disease, graft-versus-host disease, Crohn's disease, CC ulcerative colitis, multiple sclerosis or cachexia. This sequence correption of the invention.

XX Sequence 182 AA;

Query Match 100.0%; Score 110; DB 8; Length 182; Best Local Similarity 100.0%; Pred. No. 2.1e-08; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Search completed: April 6, 2006, 10:19:09 Job time : 25.2763 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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OM protein - protein search, using sw model

6, 2006, 10:19:38 ; Search time 3.81579 Seconds April Run on:

(without alignments) 504.309 Million cell updates/sec

US-10-717-984-23 Title: Perfect score:

110 1 FKDPNAPKRLPSAFFLFCSE 20 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nonhistone chromos	non-histone chromo	high mobility grou	nonhistone chromos	nonhistone chromos	high-mobility grou	nonhistone chromos	nonhistone chromos	high mobility grou	high mobility grou	HMG-1 - chicken	nonhistone chromos	gene HMG-T2 protei	nonhistone chromos	nonhistone chromos	high-mobility-grou	high mobility grou	ator	probable high mobi	mobj.	high mobility grou	mobility	dorsal switch prot	nonhistone chromos					
SUMMARIES		57	53	H	47	56	97	88	55	21	29	14	H2	19	74	10	54	59	67	62	19	90	71	11	81	20	91	40	79	89
S		S29857	A27853	NSRTH1	S01947	802826	A28897	148688	862355	830221	JC1129	JC1114	NSHUH2	A34719	S54774	D61510	150254	822359	151067	S26062	A24019	848708	T01071	B61611	T09581	B47150	S18991	T03640	JC6179	820068
	DB	~	~	Н	Ч	~	~	~	~	N	~	~	-	~	~	~	~	~	(7	~	7	~	~	~	~	~	7	N	7	7
	Length	216	170	215	215	215	215	215	210	186	207	207	209	210	210	49	201	202	215	205	172	204	204	186	141	157	161	168	393	393
de	당선	100.0	93.6	93.6	•	93.6	3	93.6	6.06	88.2	88.2	88.2	88.2	88.2	88.2	86.4	84.5	84.5		80.9	79.1	79.1	79.1			70.0	70.0	70.0	69.1	69.1
	Score	110	103	103	103	103	103	103	100	97	97	97	97	97	97	95	93	93	91	89	87	87	87	84	79	77	77	77	16	9/
	Result No.	7	8	e	4	2	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	58	29

RESULT 2

A27553
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
c)Species: Cricetulus griseus (Chinese hamster)
C;Species: Cricetulus griseus (Chinese hamster)
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A2785:
R;Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Ttle: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA sp.
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: "MRNA
A;Residues: 1-170 cLBE>
A;Residues: 1-170 cLBE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UP100001771D5
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Reywords: chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) cHMG1>
F;47-121/Domain: HMG box homology (HMG2>)

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Gaps

Query Match 93.6%; Score 103; DB 2; Length 170; Best Local Similarity 95.0%; Pred. No. 6.6e-09; Matches 19; Conservative 0; Mismatches 1; Indels 0;

high mobility grou	high mobility grou	high mobility grou	high mobility grou	HMG protein (impor	high mobility grou	probable HMG prote	mobility	high mobility grou	high mobility grou	HMG protein 1.1 -	hypothetical prote	HMG1 protein - sea	nonhistone chromos	high mobility grou	high mobility grou
T03375	T07377	T02252	\$22309	T51159	839556	F84553	T51596	\$40302	S40122	T43006	T27004	JC4357	A35072	T04662	T51598
8	N	N	N	7	7	~	~	~	N	N	N	~	~	~	7
126	141	142	152	178	149	138	138	144	154	95	312	200	93	125	141
68.2	68.2	68.2	68.2	67.3	66.4	65.5	65.5	65.5	65.5	6.09	6.09	0.09	58.2	58.2	58.2
75	75	75	75	74	73	72	72	72	72	67	67	99	64	64	64
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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Claces on 129857
Ristros, M.; Dixon, G.H.
Biochim. Blophys. Acta 1172, 231-235, 1993
A; Title: A retropeeudogene for non-histone chromosomal protein HMG-1.
A; Title: A retropeeudogene for non-histone chromosomal protein HMG-1.
A; Reference number: S29857; MUID:93176821; PMID:8439568
A; Accession: S29857
A; Molecule type: DNA
A; Residues: 1-216 <STR>
A; Accession: 1-216 <STR>
A; Residues: 1-216 <STR>
A; Note: the authors did not translate the codon for residue 1
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Reywords: chromosomal protein HMG-2; HMG box homology
F; 6-83/Domain: HMG box homology <HMG1>
F; 92-166/Domain: HMG box homology <HMG2>
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nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
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A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN:Cr. R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W. Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W. A;Title: 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2. A;Reference number: A61611; MUID:81138848; PMID:7202717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A;Residues: 2.22, %.24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Residues: 2.22, %.24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Cross-references: UNIPARC: UPI0000173987; UNIPARC: UPI0000173988
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FRBS Lett. 267, 139-141, 1990
A;Fitle: High mobility group proteins 1 and 2 bind preferentially to brominated poly (GG-cA;Reference number: S10726; MUID:90306387; PMID:2365081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: 191959
A; Molecule type: protein
B; Pentecost, B.T.; Dixon, G.H.
B; Dentecost, B.T.; Dixon, G.H.
B; Dentecost, B.T.; Dixon, G.H.
B; Pentecost, G.H.
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A;Molecule type: mRNA
A;Residues: 1-215 <MENA
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Blectrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma prot
A;Reference number: A33178; MUID:91176935; PMID:2079031
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Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
                                                   R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length CDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
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C;Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: $02826; A33178; $\overline{G}33178
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C; Accession: S01947; A61611; S10959; 145910
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A,Residues: 2-13, XXF' <WAR>
A;Cross-references: UNIPARC:UPI00001771D7
A;Accession: G33178
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Matches 19; Conservative
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A; Residues: 1-215 < KAP>
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A;Accession: A30188
A;Accession: A30188
A;Accession: A30188
A;Accession: A30188
A;Accession: A30188
A;Cross-references: Uniparc:Upi0000173985
A;Cross-references: UNIPARC:Upi0000173985
A;Cross-references: UNIPARC:Upi0000173985
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced A;Reference number: A48771; MUID:93374971; PMID:8366113
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(S.Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAT>
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S01947
nonhistone chromosomal protein HMG-1 - bovine
NyAlternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
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A;Residues: 98-105, X'. 107-112 <PA2>
A;Cross-references: UNIPARC:UP10000173986
A;Experimental source: postnatal brain
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F;92-166/Domain: HMG box homology <HMG2>
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A; Status: preliminary
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RR2>
A;Cross-references: UNIPARC:UP100000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PII
C;Genetics:
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EMBO J. 15, 548-561, 1996
A.Title: Bvidence for a shared structural role for HMG1 and linker histones B4 and H1 in A; Recession: S62355
A.Status: preliminary: nucleic acid sequence not shown A; Molecule type: mRNA
A.Residues: L-210 <NUS
A.Residues: 1-210 <NUS
A.Re
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Nucleic Acids Res. 20, 6413, 1992
Nucleic Acids Res. 20, 6413, 1992
Nucleic Acids Res. 20, 6413, 1992
A; Aftile: A human HWG2 CDNA with a novel 3'-untranslated region.
A; Reference number: S30221; MUID:93117123; PMID:1475204
A; Accession: S30221
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                                                                 A; Title: Molecular cloning, expression analysis, and chromosomal localization of A; Reference number: IS7021; MUID:94235965; PMID:8180479
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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90.0%; Pred. No. 2.4e-08;
tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 93.6%; Score 103; DB 2; Local Similarity 95.0%; Pred. No. 8.3e-09; les 19; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high mobility group protein 1 - African clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                               A; Accession: I57021
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Best Local S:
Matches 18
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C. Species: Mus musculus (house mouse)
C. Date: 0.2-011-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C. Date: 0.2-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
R. Yotov, W. V.; St. Arraud, R.
Nucleic Acids Res. 20, 3516, 1992
A. Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc
A. Residues: 14868
A. Residues: 1-215 cRES
A. Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808, 1994
A. Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A. Residues: Dreliminary; not compared with conceptual translation
A. Status: preliminary; not compared with conceptual translation
A. Residues: 1-189, E., 191-215 cFER>
A. Cross-references: UNIPARC: UDI000016CDD6; EMBL: X80457; NID:g620097; PIDN: CAA56631.1; PIR: R. Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
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ADAR897

Nonhistone chromosomal protein HMG-1 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: A28897

R;Tsuda, K; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.

Biochemistry 27, 6159-6163, 1988

A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequent A;Reference number: A28897; MUID:89050965; PMID:3191113
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A; Residues: 1-215 < rESU.
A; Residues: 1-215 < rESU.
A; Cross-references: WIPPROT: P12682; UNIPARC: UPI000016C6C4; GB: M21683; GB: M21684; NID: 916
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Superfamily: nonhistone chromosomal protein; DNA binding; nucleus
F; 6-84) Domain: HMG box homology < HMG1>
F; 992-166/Domain: HMG box homology < HMG2>
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A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UP100001771D7
C;Genetics:
A;Genetics:
A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG2>
F;92-166/Domain: HMG box homology <HMG2>
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FKDPNAPKRPPSAFFLFCSE 108
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Matches 19; Conservative
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A; Molecule type: DNA
A; Residues: 2-209 <SHI>A; Residues: 2-209 <SHI>A; Cross-references: UNIPROT: P26583; UNIPARC: UP1000012CA25; GB: M83665; NID: 9184235; PIDN: IA; Note: initiator met not shown
A; Note: initiator met not shown
R; Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, Majumdar, A.; Seidman HMG2 CDNA.
A; Title: Sequence of human HMG2 CDNA.
A; Fitle: Sequence of human HMG2 CDNA.
A; Reference number: $20061; MUID: 92093633; PMID: 1754403
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C,Species: Sus scrofa domestica (domestic pig)
C,Species: Sus scrofa domestica (domestic pig)
C,Bate: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C,Accession: A34719
R,Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A,Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nuclect A,Accession: A34719; MUID:90275208; PMID:2350545
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high mobility group 2 protein - mouse
high mobility group 2 protein - mouse)
C;Species: Mus musculus (house mouse)
C;Species: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
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A;Cross-references: GDB:119451; OMIM:118880
A;Cross-references: GDB:119451; OMIM:118880
A;Map position: 7pter-7qter
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Superfamily: nonhistone chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
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Pred. No. 7.2e-08;
0; Mismatches 1; Indels
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                        R;Shirakawa, H.; Yoshida, M.

Balol. Chem. 267, 6641-6645, 192

A;Title: Structure of a gene coding for human HMG2 protein.

A;Reference number: A42425; MUID:92202209; PMID:1551873
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88.2%; Score 97; DB 1; I

Best Local Similarity 94.7%; Pred. No. 7.2e-08;

Matches 18; Conservative 0; Mismatches 1.
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C; Accession: A42425; S20061; S18068
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Best Local Similarity 94.7%;
Matches 18; Conservative
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A; Residues: 1-209 < MAJ>
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A; Residues: 1-210 <SHI>
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Migh-mobility group protein 2 - chicken

Cispecies: Gallus gallus (chicken)

Cispecies: Gallus gallus (chicken)

Cipate: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

Cipates: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

Cipates: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

Ribavis: D.L.; Burch, J.B.E.

Gene 113, 251-256, 1992

A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt
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A; Residues: 1-207 - CDAV.
A; Cross-rences: UNIPROT: P26584; UNIPARC: UPI0000171347; GB: M83235; NID: G211926; PIDN:
C; Comment: The high mobility group proteins are among the most abundant nonhistone chrom
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-207 <SPA>
A; Residues: 1-207 <SPA>
A; Cross-references: UNIPOT: P26584; UNIPARC: UPI0000171348; GB: M80574; NID: g211928; PIDN: C; Superferantly: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords: chromosomal protein; DNA binding; nucleus
F; 6-83/Domain: HMG box homology <HMG1>
F; 92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                        nonlistence chromosomal protein HWG-2 - chicken nonhistence chromosomal protein HWG-2 - chicken nonhistence chromosomal protein 2 () Species: Gallus gallus (chicken) () Species: Gallus gallus (chicken) () Species: OS-War-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004 () Accession: JC1129; Wells, J.R.E. Gene 114, 289-290, 1992 () A.F.E. Gene 114, 289-290, 101129; MUID:92290291; PMID:1601311
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                              Gaps
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                               Length 186;
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                            Score 97; DB 2; I
Pred. No. 6.4e-08;
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88.2%; Score 97; DB 2; I
Best Local Similarity 94.7%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 1;
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C;Keywords: DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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                        Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
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Query Match

Best Loca Matches

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RESULT 11

RESULT 12

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A.Title: High mobility, group protein 2 functionally interacts with the POU domains of of A.Reference number: S54774, MUID:95237201; PMID:7720710
A.Accession: S54774
A.Accession: S54774
A.Status: preliminary; nucleic acid sequence not shown
A.Status: preliminary; nucleic acid sequence not shown
A.Residues: 1-210 <ZWINA
A.Residues: 1-210 <ZWINA
C.SSETEFERENCES: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:246757; NID:g609168; PIL
C.SUperFareferences: UNIPACT:P30681; DIPARC:UPI000016432C; FMG box homology
F.6-83/Domain: HMG box homology <HMG1>
F.92-166/Domain: HMG box homology <HMG2>
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14, 1198-1208, 1995
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RESULT 15

bi61510

high mobility group protein 1 - African clawed frog (fragment)

c;Species: Xenopus laevis (African clawed frog)

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C;Accession: D61510

C;Accession: D61510

C;Accession: D61510

C;Accession: D61510

A;Grossberger, D.; Plajnik, M.; Marcuz, A.

Comp. Biochem: Physiol: B 98, 127-133, 1991

A;Title: Ribosomal and chromosomal protein cDNA clones of Xenopus laevis thymus isolated

A;Reference number: A61510; MUID:91284580; PMID:2060276

A;Accession: D61510
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-49 < GRO>
A;Cross-references: UNIPROT:Q7LZL5; UNIPARC:UP100001771D3
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology

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Gaps

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Query Match 86.4%; Score 95; DB 2; Length 49; Best Local Similarity 89.5%; Pred. No. 3.5e-08; Matches 17; Conservative 1; Mismatches 1; Indels

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Search completed: April 6, 2006, 10:26:17 Job time : 3.81579 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model Run on: April 6, 2006, 10:13:48 ; Search time 23.6184 Seconds

(without alignments)
597.439 Million cell updates/sec
ie: US-10-717-984-23

Derfect score: 110 Sequence: 1 EXDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Uniprot_05.80:* 1: uniprot_sprot:* 2: uniprot_trembl:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8bq02 mus musculu	Q80yz1 mus musculu	Q90228 ambystoma m	Q5t7c1 homo sapien	Q5t7c2 homo sapien	homo	рошо	Q59gw1 homo sapien	พุนธ ก	P07156 cricetulus	Q8bnm0 mus musculu	Q5t7c5 homo sapien	Q5bkg1 mus musculu	Q9nqj4 homo sapien	Q6p4n5 xenopus tro	Q7sz42 xenopus lae	P10103 bos taurus	Q6yka4 canis famil	P09429 homo sapien	P63158 mus musculu	P12682 sus scrofa	rattus	gallı	Q14321 homo sapien	homo	macac	O88611 spalax leuc	O88612 spalax leuc			Q548r9 rattus norv
SUMMAKIES	ID	Q8BQ02 MOUSE	Q80YZ1_MOUSE	Q90228 AMBME	QST7C1 HUMAN		QST7C4_HUMAN	QST7C6_HUMAN	Q59GW1_HUMAN	Q8C7C4_MOUSE	HMG1_CRIGR	Q8BNM0 MOUSE	Q5T7C5 HUMAN	Q5BKQ1_MOUSE	Q9NQJ4_HUMAN	Q6P4N5 XENTR	Q7SZ42_XENLA	HMG1 BOVIN	HMG1_CANFA	HMG1_HUMAN	HMG1_MOUSE	HMG1_PIG	HMG1_RAT	Q9PUK9_CHICK	Q14321 HUMAN	QST7C3_HUMAN		O88611_SPAEH	O88612_SPAEH	Q9QWY6_SPAEH	Q9QX40_SPAEH	Q548R9_RAT
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QS8EV5_MOUSE Q9YH06_CHICK	Q6NX86_BRARE Q7ZVC6_BRARE	O4RRH9_TETNG O91596_XENLA	OGGNOS_XENLA	HMG1X HUMAN	Q9CT19 MOUSE	Q96J53_HUMAN	Q6Y235 PAGMA	HMG4 CHICK	HMG2_CHICK	HMG2_HUMAN
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215	205	199	210	211	190	195	200	201	206	208
93.6	91.8 91.8	90.9	6.06	90.9	88.2	88.2	88.2	88.2	88.2	88.2
103	101	100	100	100	97	97	97	97	97	97
32 33	34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mayashizaki Y., Hasegawa Y., Kawaji H., Kohtsuki S., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN=CS7BL/6J; TISSUE=Spinal ganglion;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUB=Spinal ganglion; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninoi P., HayAshliaski Y.; High-efficiency full-length cDNa cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:D130095009 product:high mobility group box 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN-C57BL/6J; TISSUE-Spinal ganglion;
MEDLINE-21085660; PubMed-11217851; DOI=10.1038/35055500;
                                                  215 AA.
                                                                                                                                       Created)
                                                  PRT;
                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                      QBBQ02_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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ORBOOL MOUSE
ORBOOL MAR-21
DT 01-MAR-22
DT 01-MAR-22
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"High levels of HMG1-2 protein expression in the cytoplasm and nucleus of hydrocortisons esnitive amphibian thymocytes.";
Biol. Cell 69:153-160(1990). mRNA.
EMBL; U31513; AAB08831.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                A Hunter G., Kimberley C., Thomas D., Cave-Berry L., Weston P.,
Botcherby M.R.M.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; ALG/0999; CAD83017.1; -; Genomic_DNA.

R SMR; G097156; 1NRN.

R SMR; G0070156; 1NRN.

R SMR; G007000064154; Mus musculus.

R G0; G0.0000785; C:chromatin; IEA.

G0; G0.0000785; C:chromatin; IEA.

G0; G0.0006357; F:DNA binding; IEA.

G0; G0.0006357; F:DNA binding; IEA.

R G0; G0.0006357; F:DNA binding; IEA.

R FINTERPRO; IPR000135; Highmoblty_12.

R InterPro; IPR000135; Highmoblty_12.

R PRINTS; PR00886; HIGHMOBLTY12.
                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=56263766, PubMed=8654668, DOI=10.1016/0145-305X(95)00025-0, de Guerra A., Guillet F., Charlemagne J., Fellah J.S.; "Identification of CDNA clones encoding HMG 2, a major protein of the mexican axolotl hydrocortisone-sensitive thymocytes."; pev. Comp. Immunol. 19:417-423(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guillet F., Tournefier A., Denoulet P., Capony J.P., Kerfourn F., Charlemagne J.;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BM168F16.1 (Novel protein similar to high-mobility group box 1
                                                                                                                                                                                                                                                                     North P., Leaves N., Greystrong J., Coppola M., Manjunath S.,
Russell E., Smith M., Strachan G., Tofts C., Boal E., Cobley V
Hunter G., Kimberley C., Thomas D., Cave-Berry L., Weston P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4DBCB7B9516D7B52 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.5%; Score 104; DB 2; Le
95.0%; Pred. No. 1.8e-08;
".ismarches 1;
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Name=HMG-2;
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Q90228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00398; HMG; 2.
                                                                          Name=bM168F16.1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                           NUCLEOTIDE SEQUENCE.
STRAIN=C5/BL/6J; TISSUB=Spinal ganglion;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                         MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Tashiro H., Itoh M., Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yujiweke S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Watshika T., Okazaki Y., Matsuura S., Kawai J., Rikiki integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI; MGI:96113; Hmgbl.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:00105615; C:extracellular space; IDA.
GO; GO:0010235; F:nitric-oxide synthase regulator activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006810; P:nitric oxide biosynthesis; IDA.
GO; GO:0006810; P:nitric oxide biosynthesis; IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8A86969266DC07F5 CRC64;
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Last sequence update)
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InterPro; IPR000910; HMG 12 box.
Pfam; PF00505; HMG box; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00886; HIGHMOBLTY12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 AA; 24905 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P07155; 1CKT.
SMR; Q8BQ02; 2-84, 93-171.
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QBOYZ1;
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  Nature 420:563-573(2002)
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                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
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RESULT 2
QBOYZ1 MO
ID QBOY
AC QBOY
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Gaps

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Length 208;

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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment).
Name-HWGB1; ORFNames-RP11-550P23.1-009;
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                              EMBL, AL353648; CAL15604.1; -; Genomic_DNA.

SMR; Q5T7C2; 2-84, 89-157.

GO; GO:000785; C:chromatin; IEA.

GO; GO:0005634; C:mucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:000357; F:DNA binding; IEA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000910; HMG 12_box.

Pfam; PF00505; HMG box; Z.

PRINTS; PR00886; HJGHMOBLTY12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AL353648; CAL15603.1; -; Genomic_DNA.

EMBL; AL353648; CALTS603.1; -; Genomic_DNA.

SNR; Q577C4; 2-84, 89-157.

GO; GO:0000785; C:chromatin; IEA.

GO; GO:0005634; C:uncleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000910; Highmoblty_12.

InterPro; IPR000910; HMG 12 box.

Pfam; PF00505; HMG box; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%; Score 103; DB 2; Length 157; 95.0%; Pred. No. 2e-08; 1; Indels 1; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 157 AA; 18164 MW; F38343E7F52FC457 CRC64;
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PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 158 AA; 18311 MW; 1A438343E7F52FC4 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
11-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-moblilty group box 1.
Name-HMGB1; ORFNames=RP11-550P23.1-003;
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PROSITE; PS50118; HMG BOX 2; 2.
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SMART; SM00398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QST7C4_HUMAN PRELIMINARY;
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00398; HMG; 2.
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Best Local Similarity
                                                                                                                                                                            NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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PIR, A60975; A60975.

R SNR; P07155; LCKT.

R SNR; A60975; LCKT.

R CO; GO: 0000785; C: chromatin; IEA.

R CO; GO: 0005634; C: chromatin; IEA.

R CO; GO: 0006377; F: DNA binding; IEA.

R CO; GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000135; Highmoblty_12.

R InterPro; IPR000135; HMG 12_box.

P Fam; PF00505; HMG box; Z.

P RINTS; PR00886; HIGHMOBLTY12.

P RINTS; PR00886; HIGHMOBLTY12.

P ROSITE; PS00135; HMG BOX 1; 1.

PROSITE; PS00118; HMG BOX_1; 1.

PROSITE; PS00118; HMG BOX_2; 2.

R ROSITE; PS00118; HMG BOX_2; 2.

R ROSITE; PS00118; HMG BOX_2; 2.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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GO; GO: 0005634; C: nucleus; IEA.

GO; GO: 0003677; P: DNA binding; IEA.

GO; GO: 0006357; P: P: Pranting; IEA.

GO; GO: 0006357; P: regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000135; Highmobity_12.

InterPro; IPR00910; HWG 12_box.

PRINTS; PR00886; HIGHMOBITY12.

SMART; SM00398; HMG; 2.
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                                                                                                                                                                                                                                                                                                                                             94.5%; Score 104; DB 2; Length 216; 100.0%; Pred. No. 1.9e-08; rive 0; Mismatches 0; Indels
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-moblity group box 1 (Fragment).
Name-HMGB1; ORFNames-RP11-550P23.1-006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 132 AA.
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SMR; QST7C1; 2-84.
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01-FEB-2005 (TrEMBLrel. 29, Created)
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PROSITE; PS50118; HMG_BOX_2; 2.
NON_TER 132 132
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Best Local Similarity 100.(
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OST7C1;
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NCBI_TaxID=9606;
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Matches

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Gaps

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Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                           01-MAR-2003
                                                                                                                                                                                                     Name=Hmgb1;
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                                                                                                               28C7C4 MOUSE
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                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S., Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                               SMR; 05T7C6; 2-84, 89-144.

GO; GO:00005834; C:chromatin; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; F:DNA binding; IEA.

GO; GO:000135; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000910; HMG 12_box.

Pfam; PF00596; HMG 22_box.

Pfam; PF00596; HMG 22_box.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 162;
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Pred. No. 2.1e-08;
0; Mismatches 1; Indels
 1; Indels
                                                                                                                                                                                                                                   Pelan S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                           162 AA.
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                                                                                                                                                                                                                                                        EMBL; AL353648; CAI15601.1; -; Genomic_DNA.
0; Mismatches
                                                                                                                                          High-mobility group box 1 (Fragment).
Name=HMGB1; ORFNames=RP11-550P23.1-002;
                                                                                        PRT;
                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                       FKDPNAPKRPPSAFFLFCSE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKDPNAPKRPPSAFFLFCSE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FKDPNAPKRLPSAFFLFCSE 20
                    FKDPNAPKRLPSAFFLFCSE 20
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SMART; SM00398; HMG; 2.

RROSITE; PS00353; HMG BOX 1; 1.

PROSITE; PS50118; HMG BOX_2; 2.

NOW TER 162 162
                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%;
                                                                                                                      01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                              01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.00,
Best Local Similarity
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Q59GW1;
                                                                                         QST7C6_HUMAN PRELIMINARY;
19; Conservative
                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   162 AA;
                                                                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nokazaki Y., Itoh M., Hayashizaki Y.; Shibata to M., Hayashizaki Y.; Dibhataki Dibhataki M., Hayashizaki Y.; Dibhataki Dibhataki M., Mormalizakion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone: C920030E14 product: high mobility group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIN=CSTBL/66; TISSUE=Thymus;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                       Gaps
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                                                                                            ..
0
        Length 176;
Score 103; DB 2; Length 17
Pred. No. 2.2e-08;
0; Mismatches 1; Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   box 1, full insert sequence. (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                              91 FKDPNAPKRPPSAFFLFCSE 110
                                                                                                                                                                               1 FKDPNAPKRLPSAFFLFCSE 20
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    93.6%;
ilarity 95.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8C7C4_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
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103 1
180 AA;
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  NCBI_TaxID=10029;
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PDB;
SMR;
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B. Shibata M. Sailli Man.

Shipata A., Muramatsu M., Hayashizaki Y.;

Shipata A., Muramatsu M., Hayashizaki Y.;

Shipata M., Hayashizaki M., Hayashizaki Y.;

Shipata M., Hayashizaki M., Hayashizaki Y.;

Shipata M., Hayashizaki M., Hayashizaki Y.;

Shipata M., Mayashizaki M., Mayashizaki M., Hayashizaki M., Mayashizaki M., M
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                                               NUCLEOTIDE SEQUENCE.

C STRAIN=C57BL/6J; TISSUB=Thymus;

MEDLINE=C0530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=C0530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
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Name=HMGBL; Synonyms=HMG-1, HMG1;
Cricctulus griseus (Chinese hamster).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Cricetulus.
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13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AA; 20303 MW; 155FD80D52960A62 CRC64;
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InterPro; IPR000910; HMG 12 box.
Pfan; PF00505; HMG box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00353; HMG BOX 1; 1. PROSITE; PS50118; HMG BOX 2; 2. NON TER
Genome Res. 10:1617-1630(2000)
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P07156;
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SEQUENCE
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HMG1_CRIGR
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                     MEDLINE=3347974; PubMed=8346022;
Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.;
"Solution structure of a DNA-binding domain from HMG1.";
"Nucleic Acids Res. 21:347-3436 (1993).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
double stranded DNA.
-!- SUBCELLUTAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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                                                                                                                      "Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle expression of the HMG-1 gene."; Nucleic Acids Res. 15:5051-5068 (1987).
NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDILINE=87259986; PubMed=3601666;
Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
Dixon G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PSS0118; HMG BOX_2; 2.
3D-structure; Chromosomal protein; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0000793; C:condensed chromosome; ISS.
GO; GO:0008301; F:DNA bending activity; ISS.
GO; GO:000510; F:Drotein binding; ISS.
GO; GO:0005288; P:Dase-excision repair, DNA ligation; ISS.
GO; GO:0006281; P:DNA recombination; ISS.
GO; GO:0006281; P:DNA repair; ISS.
GO; GO:0006281; P:DNA unwinding; ISS.
GO; GO:0006282; P:establishment and/or maintenance of chromat.
GO; GO:0006325; P:negative regulation of transcriptional prei.
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HMG box 2.
Asp/Glu-rich (acidic)
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InterPro, IPR000910; HMG 12_box.
Pfam; PF00505; HMG_box; 2.
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                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 57-136
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1HSN, NWR; @=58-136.
1NHM; NWR; @=58-136.
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Best Local Similarity 95.0
Matches 19; Conservative
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RESULT 12
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                                                                   ol-mar-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
library, clone:C430013M12 product:high mobility group box 1, full
namet sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=CSTBL/60; TISSUE=Whole body;
STRAIN=CSTBL/60; TISSUE=Whole body;
STRAIN=CSTBL/60; TISSUE=Whole body;
SHIDNE=Z0530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
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The FANTOM Consortium,
                                      QBBNMO MOUSE PRELIMINARY;
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                                                                                                                                                                        Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                              Name=Hmgb1;
                          MOUSE
         RESULT 11
QBBNM0_MOU
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C STRAIN=C57BL/6J; TISSUB=Whole body;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Arunda S., Furuno M., Hansgaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hori F., Imotami K., Ishii Y., Itoh M., Kagawa T., Kada M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Ohasto N., Okazaki Y., A Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasti D., Shibate K., Shibata R., Shiraki T., Soqabe Y., Tagami M., A Tagawa A., Taya T., Yakaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (Apr-2002) to the BMBL/Genbank/DDBJ databases.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Miramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikibi integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003235; F:nitric-oxide synthase regulator activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006810; P:transport; IDA.
HIACETO: IRRO00135; Highmoblty 12.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box; Z.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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Name=HMGB1; ORFNames=RP11-550P23.1-001;
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MGI:96113; Hmgbl.
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Best Local Similarity 95.0°
Matches 19, Conservative
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SMART; SM00398; HMG; 2.
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NUCLEOTIDE SEQUENCE.
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SEQUENCE
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us-10-717-984-23.rup

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206 AA; 23569 MW; 3F06A32D1A618B98 CRC64;
        Hypothetical protein. SEQUENCE 206 AA; 2
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000130; Highmoblty_12.
PinterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box; Z.
PRINTS; PR00886; HTGHMOBLTY12.
SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS01319; HMG_BOX_2; 2.
NON_TER 192 192
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC09089; AAH90899.1; -; mRNA.
InterPro; IPR0101486; HdeA.
InterPro; IPR010135; Highmoblty 12.
InterPro; IPR010191; HMG 12 box.
InterPro; IPR011991; PH type.
InterPro; IPR011991; PH type.
InterPro; IPR011991; Wing ht bd.
Pf00505; HMG box; 2.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 95.03
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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OSBROIL MOUNT
DE 10-MA
DT 10-MA
DE MUSTE
RA MISELI
RA RADIA
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RA BLOW
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RA BLAKE
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                           Gaps
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GO; GO:00005634; C:nucleus; IEA.
GO; GO:00005634; F:DNA binding; IEA.
GO; GO:0006357; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000130; HMG Dox; Z.
Pfam; PF00505; HMG Dox; Z.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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93.6%; Score 103; DB 2; Length 211;
Best Local Similarity 95.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels
Length 206;
                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howden P.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL160176; CAB92731.1; -; Genomic_DNA.
HSSP; P07155; IHWF.
SMR; Q9NQJ4; 2-84, 93-171.
Ensembl; ENSG0000124997; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan: PF00505; HWG box; Z.
PRINTS; PR0086; HTGHWOBLTY12.
SMART; SM00398; HMG; 2.
PR051TE; PS0118; HMG; BOX 2; 2.
SEQUENCE 211 Aa; 24238 WW; D2623FDE00FA8355 CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OTTHUMPO0000031372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JJJ-2004 (TrEMBLrel. 27, Created)
05-JJJ-2004 (TrEMBLrel. 27, Last sequence update)
05-JJJ-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC75695.
  Query Match
93.6%; Score 103; DB 2;
Best Local Similarity 95.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                            211 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=HMG1L1; ORFNames=RP4-579F20.2-001;
Homo sapiens (Human).
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                                                                                                                                                89 FKDPNAPKRPPSAFFLFCSE 108
                                                                                                                 1 FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                                                             RESULT 14
Q9NQJ4 HUMAN
ID Q9NQJ4 HUMAN PRELIMINARY;
AC Q9NQJ4-7000 (TFRMELEE). 15
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QGF4MS. XENTR
ID QGP4MS, XENTR PRELIMINARY;
AC QGP4MS;
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TISSUE=Embryo;
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RX MEDIATES-218257; PubMed-124773; DOI-10.1073/pnas.24263399;
RX Atlauener R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Atlauener R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B. B., Woore T. Wax S.I., Wang L.,
RA Atlauener R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Atlauener R.D., Colling F.S., Wagner L., Shemen C.M., Schuler C.D.,
RA Bachesko L., Warusina K., Farmer A.A., Rubin GM., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheeter T.E.,
RA Manas. S.A., McDena P.J., Workstran K.J., Abramson R.D., Mullaby S.J.,
RA Michies D. K., Mullan P.J., Soderer G.J., Abramson R.D., Mullaby S.J.,
RA Michies D. K., McTen R., Soderer G.J., Abramson R.D., Mullaby S.J.,
RA Mithing M. Madan A., Young A.C., Shaveherky Y., Bonitard G.G.,
RA Mithing W. Madan A., Young A.C., Shaveherky Y., Bonitard G.G.,
RA Mithing W. Madan A., Young A.C., Shaveherky Y., Bonitard G.G.,
RA Mithing W. Madan A., Young A.C., Shaveherky Y., Bonitard G.G.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Media S., Gerhard D.S.;
RA Media S., Gerhard
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6, 2006, 10:25:15

Search completed: April Job time: 26.6184 secs

FKDPNAPKRPPSAFFLFCSE 108

Run ĕ

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Ozaki, Shoichi
Sobajima, Junko
Usaugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
Yoshida, Michiteru
Shirakawa, Hitoshi
Osakada, Fumio
 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
US-09-214-881A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 883
LENGTH: 214
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 FEATURE
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Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 1018, Ap
Sequence 2, Appli
Sequence 6, Appli
Sequence 10728, A
Sequence 10728, A
Sequence 4826, Ap
Sequence 324, App
                                                                                                                      (without alignments)
288.890 Million cell updates/sec
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                                                                                                      April 6, 2006, 10:25:39 ; Search time 5.72368 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-214-881A-1
US-09-214-881A-3
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US-09-214-881A-5
US-09-214-881A-2
US-09-214-881A-2
US-09-214-881A-8
US-09-213-999C-4826
US-09-513-999C-4826
US-09-513-999C-4826
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Maximum Match 100%
Listing first 45 summaries
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1 FKDPNAPKRLPSAFFLFCSE 20
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Sequence 324, App
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Sequence 789, App
Sequence 1667, App
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; Sequence 883, Application US/09538092
; Patent No. 6753314
; Patent No. 6753314
; Patent No. 6753314
; APPLICANT: Giot, Loic
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same; PILE REPERBNCE: 15966-542
; CURRENT FILING DATE: 2000-03-29
; PRIOR PILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
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; OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883
                                                US-10-017-754-324
US-10-017-754-324
US-09-651-563-334
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US-09-519-642-324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FKDPNAPKRLPSAFFLFCSE 20
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Sequence 5, Application US/09214881A Patent No. 6822078
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1999-06-07
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nes 19; Conservative
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                                                                                                                                                                                                ; ORGANISM: Sus scrofa
US-09-214-881A-4
   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-10813
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SEQ ID NO 5
LENGTH: 214
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APPLICANT: Sobajima, Junko
APPLICANT: Genergi, Hiroko
APPLICANT: Genergi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Noshida, Michiteru
APPLICANT: Sobalda, Michiteru
APPLICANT: Sobakada, Hiroshi
APPLICANT: Osakada, Fumio
TILLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0.104
CURRENT APPLICATION NUMBER: US/09/214,881A
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APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 063383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.6%; Score 103; DB 2; Length 214; Best Local Similarity 95.0%; Pred. No. 5.2e-09; Matches 19; Conservative 0; Mismatches 1; Indels
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                        FILE REFERENCE: 068383.0104

CURRENT APPLICATION NUMBER: US/09/214,881A

CURRENT FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 214

TYPE: PTP: PTP: TYPE: T
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Sobajima, Junko
Usaugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
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Best Local Similarity 95.03
Matches 19; Conservative
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APPLICANT: Ocaki, Sh
APPLICANT: Ocaki, Sh
APPLICANT: Ocacyi, H
APPLICANT: Tanaka, M
APPLICANT: Tanaka, M
APPLICANT: Nakao, Kai
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ORGANISM: Bos taurus
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SOFTWARE: PATE
SEQ ID NO 3
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US-09-214-881A-3
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US-09-214-881A-4
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 10813, Application US/09949016

Sequence 10813, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10813
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93.6%; Score 103; DB 2; Length 214; 95.0%; Pred. No. 5.2e-09; Live 0; Mismatches 1; Indels
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; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
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i Sequence 1018, Application US/09538092
; Patent No. 675314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REPERENCE: 1596-542
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 05/127,352
; PRIOR PILING DATE: 1999-01
; PRIOR PILING DATE: 1999-01
; PRIOR FILING DATE: 1999-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1018
; LENGTH: 208
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APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Gaskada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPRENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
                                                                                                90.9%; Score 100; DB 2; Length 213; ilarity 94.7%; Pred. No. 1.6e-08; Conservative 0; Mismatches 1; Indels
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APPLICANT: Sobajima, Junko
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masa
APPLICANT: Nakao, Kasuwa
APPLICANT: Noshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
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ORGANISM: Gallus gallus
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ORGANISM: Homo sapiens
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LOCATION: (0)...(0)
                                                                                                  Query Match
Best Local Similarity
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                   ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10813
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LENGIH: 206
LENGTH: 213
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APPLICANT: OKAZAKI, TAKANIKO

APPLICANT: OKAZAKI, TAKANIKO

APPLICANT: TANAKA, MASSAO

APPLICANT: TANAKA, MASSAO

APPLICANT: Shirakawa, Hitoshi

APPLICANT: Osakada, Fumio

TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES

FILE REFERENCE: 06383.0104

CURRENT APPLICATION NUMBER: US/09/214,881A

CURRENT FILING DATE: 1999-06-07

NUMBER, OF SEQ ID NOS: 13

SEQ ID NO 2

LENGTH: 208
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usazaki, Hirkako
APPLICANT: Usazaki, Hakahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT PELLING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
LENGTH: 209
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Score 97; DB 2; Pred. No. 4.8e-08; 0; Mismatches 1
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Pred. No. 4.8e-08;
0; Mismatches 1
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  Query Match 88.2%;
Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity 94.7%;
Matches 18; Conservative
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APPLICANT: Ozaki, Shoichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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0; Mismatches
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                              201 KDPNAPKRPPSAFFLFCSE 219
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    2 KDPNAPKRLPSAFFLFCSE
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Best Local Similarity 90.03
Matches 18; Conservative
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Matches 18; Conservative
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CRGANISM: Homo sapiens
US-09-914-259-38
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ORGANISM: Homo sapiens
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US-09-949-016-10728

Sequence 10728, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISNS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER: FastSEQ ID NOS: 207012

SEQ ID NO 10728
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Patent No. 6822078

GENERAL INFORMATION.

APPLICANT: Ozaki, Shoichi

APPLICANT: Ozaki, Takahiro

APPLICANT: Okasaki, Takahiro

APPLICANT: Okasaki, Takahiro

APPLICANT: Tanaka, Masao

APPLICANT: Yoshida, Michiteru

APPLICANT: Yoshida, Michiteru

APPLICANT: Shirakawa, Hitoshi

APPLICANT: Shirakawa, Hitoshi

APPLICANT: Osakada, Fumio

ITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES

FILE REFERENCE: 068383.0104

CURRENT FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 8

LENGTH: 209
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/ Match 88.2%; Score 97; DB 2; Length 209; Local Similarity 94.7%; Pred. No. 4.8e-08; nes 18; Conservative 0; Mismatches 1; Indels
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94.7%; Pred. No. 7.7e-08;
ive 0; Mismatches 1; Indels
                                                                                                                   89 KDPNAPKRPPSAFFLFCSE 107
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                                                                                  2 KDPNAPKRLPSAFFLFCSE 20
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Best Local Similarity 94.7
Matches 18; Conservative
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US-09-949-016-10728
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Sequence 4826, Application US/09513999C

Patent No. 6783961

GENERAL.INFORMATION:
APPLICANT: Dunas Mine Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

FILE REFRENCE: 59. US2.REG
CURRENT APLICATION NUMBER: US 60/122,487

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 4826

LENGTH: 59
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Sequence 38, Application US/09914259
Fatent No. 6495336
GENERAL INFORMATION:
APPLICANT: HAMAN, Paul
APPLICANT: Williams, Mark
TITILE REFERENCE: 8471-010-999
CURRENT FILION NUMBER: US/09/914,259
CURRENT FILION DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 879
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90.09-513-99C-4824
$$ Sequence 4824, Application US/09513999C
$$ Patent No. 6783961
$$ GENERAL INFORMATION:
$$ APPLICANT: Dumas Milne Edwards, J.B.
$$ APPLICANT: Duclert, A.
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HITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PAPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SOFTWARE: NUMBER: US 60/122,487
CORGANISM: Homo sapiens
FRATURE:
NAME/KEY: UNSURE
COCATION: 91
COTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824
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Best Local Similarity 90.0%; Pred. No. 3.5e-08;
Matches 18; Conservative 0; Mismatches 2; Indels
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Search completed: April 6, 2006, 10:27:51 Job time : 6.72368 secs

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RESULT 2
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(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-30-072-23
US-10-456-947-45
US-10-456-947-45
US-10-717-944-23
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US-10-300-072-53
US-10-300-072-53
US-10-300-072-53
US-10-456-947-8
US-10-456-947-8
US-10-718-495-20
US-10-718-495-20
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Listing first 45 summaries
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1 FKDPNAPKRLPSAFFLFCSE 20
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Maximum DB seq length: 2000000000
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Publication No. US20030144201A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
APPLICANT: Huan Yang
APPLICANT: Huan Yang
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
FILE REPERENCE: 3269.1001-005
CURRENT APPLICATION NUMBER: US/10/300,072
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US/10/47,447
PRIOR PILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,034
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SQUENCE 16, Application US/10147447

Publication No. US20030060410A1

GENERAL INFORMATION:
APPLICANT: Tracey, Kevin J.
APPLICANT: Yang, Huan
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Fink, Mitchell P.
TITLE OF INVENTION: Use of HMG Fragments as
TITLE OF INVENTION: Anti-Inflammatory Agents
FILE REPERENCE: 3268.1001-001
CURRENT APPLICATION NUMBER: US/10/147,447

CURRENT FILING DATE: 2002-08-16

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20

LENGTH: 20
US-10-456-947-6
US-10-718-495-18
US-10-718-495-18
US-10-717-984-18
US-10-717-984-24
US-10-938-992-1
US-10-300-072-54
US-10-300-072-54
US-10-300-072-54
US-10-300-072-54
US-10-300-072-54
US-10-300-072-54
US-10-456-947-40
US-10-718-495-54
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ORGANISM: Homo sapiens
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Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
         ; ORGANISM: Homo Sapiens
US-10-456-947-45
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ORGANISM: Homo sapiens
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US-10-717-984-23
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US-10-147-447-20
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US-10-456-947-45

i Sequence 45, Application US/10456947

j Publication No. US20040053841A1

j GENERAL INFORMATION:
   APPLICANT: Kevin J. Tracey

j APPLICANT: Huan Yang

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

CURRENT FILING DATE: 2001-06-06

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 45

LENGTH: 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-456-949-16

Sequence 16, Application US/10456949

Publication No. US20040005316A1

GENERAL INFORMATION:

APPLICANT: Revin J. Tracey

APPLICANT: Huan Yang

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

FILE REFERENCE: 3268-1001-006

CURRENT FILING DATE: 2003-06-16

PRIOR APPLICATION NUMBER: 10/147,447

PRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FRAELSC for Windows Version 4.0
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 20
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ORGANISM: Homo sapiens
US-10-300-072-23
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 20; Conserv
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LENGTH: 20
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    Length 20;
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; Score 110; DB 4;
; Pred. No. 2.4e-09;
0; Mismatches 0;
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| Publication No. US20040156851A1
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| TITLE OF INVENTION: HMGBL COMBINATION THERAPIES
| TITLE OF INVENTION: HMGBL COMBINATION THERAPIES
| CURRENT FILING DATE: 2003-11-20
| PRIOR PAPLICATION NUMBER: US/10/717,984
| PRIOR APPLICATION NUMBER: 60/427,846
| PRIOR FILING DATE: 2002-11-20
| NUMBER OF SEQ ID NOS: 58
| SEQ ID NO 23
| LENGTH: 20
| TYPE: PAPE |
| ORGANISM: Homo sapiens
| US-10-717-984-23
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Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0;
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US-10-718 495-23
US-10-718 495-23
Sequence 23, Application US/10718495
Publication No. US20040141948A1
GENERAL INFORMATION:
APPLICANT: O'KEEFE, Theresa L.
TITLE OF INVENTION: USE OF HAGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR PRIOR DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 23
LENGTH: 20
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Sequence 8, Application US/10456947
Publication No. US20040053841A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
TITLE OF INVENTION: ANII-INFLAMMATORY AGENTS
FILE REPERENCE: 3268.1001-007
CURRENT APPLICATION NUMBER: US/10/456,947
                  APPLICANT: Matchell P. Fink
TITLE OF INVENTION: GEOF HWGB FRAGMENTS AS ANTI-FLAMMATORY
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 3260-1001-005
CURRENT APPLICATION NUMBER: US/10/300,072
CURRENT PILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-05-15
PRIOR PELLING DATE: 2002-05-15
PRIOR PELLING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 53
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 20, Application US/10456949
Publication No. US20040005316A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REPERENCE: 3268.1001-006
CURRENT APPLICATION NUMBER: US/10/456,949
CURRENT FILING DATE: 2003-06-06
FRIOR FILING DATE: 2002-05-15
FRIOR FILING DATE: 2002-05-15
FRIOR FLING DATE: 2002-05-15
FRIOR FLING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FREESEQ for Windows Version 4.0
  Howland Shaw Warren, Jr.
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US-10-456-949-20
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LENGTH: 74
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US-10-300-072-20

Sequence 20, Application US/10300072

Sequence 20, Application US/10300072

Publication No. US20030144201A1

GENERAL INFORMATION:

APPLICANT: Huan Yang

APPLICANT: Howland Shaw Warren, Jr.

TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY

TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY

TITLE OF INVENTION: USE OF HMGB FRAGMENTS

FILE REFERENCE: 3268.1001-005

CURRENT APPLICATION NUMBER: US/10/300,072

CURRENT PILING DATE: 2002-11-20

PRIOR FILING DATE: 2002-11-20

PRIOR PILING DATE: 2001-05-15

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 74
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100.0%; Pred. No. 9.6e-09;
tive 0; Mismatches 0;
                                                                    APPLICANT: Yazeey, Kevin J.
APPLICANT: Yarg, Huan
APPLICANT: Yarg, Huan
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Fink, Mitchell P.
TITLE OF INVENTION: Use of HMG Fragments as
TITLE OF INVENTION: Anti-Inflammatory Agents
FILE REPERSENCE: 3268.1001-001
CURRENT APPLICATION NUMBER: US/10/147,447
CURRENT FILING DATE: 2002-08-16
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 20, Application US/10147447 Publication No. US20030060410A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 20; Conservative
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CRGANISM: Homo sapiens
US-10-147-447-20
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ORGANISM: Homo sapiens
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Best Local Similarity
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Search completed: April 6, 2006, 10:32:46
                         ORGANISM: Homo sapiens US-10-718-495-20
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; TYPE: PRT
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Sequence 39, Application US/10456947

Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Huan Yang

TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: Hugh POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: Hugh POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: Hugh POLVEPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: Hugh POLICATION NUMBER: US/10/456,947

CURRENT FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: 10/147,447

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PASISEQ for Windows Version 4.0

LENGTH: 74
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Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 20, Application US/10718495

Publication No. US20040141948A1

GENERAL INFORMATION:

TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS

TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

CURRENT APPLICATION NUMBER: US/10/718,495

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: 60/427,841

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PASLSEQ for Windows Version 4.0

SEQ ID NO 20
            PRIOR APPLICATION NUMBER: 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 74
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2003-06-06
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapiens
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; ORGANISM: Homo Sapiens
US-10-456-947-39
CURRENT FILING DATE:
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US-10-456-947-39
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US-10-718-495-20
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Query Match
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
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Publication No. US20040156851A1

GENERAL INFORMATION

APPLICANT: Newman, Walter

TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES

FILE REFERENCE: 3288.1008-001

CURRENT APPLICATION NUMBER: US/10/717,984

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR PRIUNG DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 20

SEQ ID NO 20

LENGTH: 74
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Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                       Sequence 53, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe I.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS; TITLE OF INVENTION UNMBER: US/10/718,495
; CURRENT APPLICATION NUMBER: 00/42',841
; PRIOR APPLICATION NUMBER: 60/42',841
; RIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FRAESEQ for Windows Version 4.0
; SEQ ID NO 53
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                                                                                                       1 FKDPNAPKRLPSAFFLFCSE 20
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Best Local Similarity 100.0
Matches 20; Conservative
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; ORGANISM: Homo sapiens
US-10-718-495-53
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1. /SIDS5/ptodata/2/pubpaa/US08_NEW PUB.pep:*
2. /SIDS5/ptodata/2/pubpaa/US07_NEW PUB.pep:*
3. /SIDS5/ptodata/2/pubpaa/US07_NEW PUB.pep:*
4. /SIDS5/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5. /SIDS5/ptodata/2/pubpaa/US09_NEW PUB.pep:*
6. /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7. /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8. /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-186-422-11

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Maximum Match 100%
Listing first 45 summaries
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1 FKDPNAPKRLPSAFFLFCSE 20
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Gapop 10.0 , Gapext 0.5
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SQUEGNCE 1443, Application US/10821234

PUBLICATION NO. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Stache-Crain, Birgit

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

CURRENT APPLICANTON NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER: OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ_Genes Version 1.0

SEQ ID NO 1443

LENGTH: 215
Sequence 15614, A Sequence 969, App Sequence 1563, App Sequence 1572, App Sequence 2564, App Sequence 370, App Sequence 10060, A Sequence 13611, A Sequence 10535, A Sequence 26883, A Sequence 2773, Ap Sequence 2773, Ap Sequence 2773, Ap
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              US-11-087-099-869
US-11-087-099-869
US-11-172-740-1563
US-11-172-740-1572
US-11-087-099-2564
US-11-087-099-10060
US-11-087-099-6594
US-11-087-099-10887
US-11-096-568A-13611
US-11-096-568A-13611
US-11-096-568A-1688
US-11-087-099-11987
US-11-087-099-11987
US-11-087-099-11987
US-11-087-099-11087
US-11-087-099-11087
US-11-087-099-11087
US-11-087-099-6977
US-11-087-099-6977
US-11-087-099-6977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WS-UL-186422-11
Sequence 11, Application US/11186422
Fublication No. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Theresa
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
FILE REFERENCE: 3258-1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT FILING DATE: 2005-07-20
FRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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Best Local Similarity 95.0'
    TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1443
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DEFICEANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
NUMBER OF SEQ ID NOS: 527
SOFTWARE: Patentin version 3.2
SEQ ID NO 192
LENGTH: 879
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Pred. No. 1.2e-07;
0; Mismatches 2; Indels
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                                                                                                 Indels
                                               Score 97; DB 6; I
Pred. No. 2.3e-08;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-186-422-14

Sequence 14, Application US/11186422

Publication No. US20060057679A1

GENERAL INFORMATION:

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: O'Keefe, Theresa

APPLICANT: Luciano, Peter

APPLICANT: Qin, Shixin

TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES

FILE REFERENCE: 3258.1021-003

CURRENT APPLICATION NUMBER: US/11/186,422

CURRENT FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: 60/589,678

PRIOR PILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 34

SOGTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 14
                                                                                                                                                                                                                                                                                US-11-169-041-192

: Sequence 192, Application US/11169041

: Publication No. US20060019284A1

; GENERAL INFORMATION:
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                                                                                                                                            2 KDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                    77 KDPNAPKRPPSAFFLFCSE 95
                                                 Query Match 88.2%;
Best Local Similarity 94.7%;
Matches 18; Conservative (
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Best Local Similarity 90.0%;
Matches 18; Conservative (
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Best Local Similarity 93.8%;
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-11-169-041-192
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       US-10-821-234-1234
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; Sequence 1234, Application US/2050551141
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: DF SEQ Genes Version 1.0
; SEQ ID NO 1234
; LENGTH: 169
; TYPE: PRI
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                                                                                                                                                              93.6%; Score 103; DB 7; Length 215; 95.0%; Pred. No. 3.2e-09; Live 0; Mismatches 1; Indels
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LOCATION: (1)...(169)
OTHER INFORMATION: Xaa = any amino acid or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CITLICAL THE THE TABLE APPLICANT: CITLICAL THE TEAS APPLICANT: O'Keefe, Theresa APPLICANT: O'Keefe, Theresa APPLICANT: O'Keefe, Theresa APPLICANT: UCIN Shixin FILE OF INVENTION: RAGE PROTEIN DERIVATIVES TILLE REPERENCE: 328.1021-003 CURRENT PAPLICATION NUMBER: US/11/186,422 CURRENT FILING DATE: 2005-07-20 PRIOR APPLICATION NUMBER: 60/589,678 PRIOR PILLING DATE: 2004-07-20 NUMBER OF SEQ ID NOS: 34 SOFTWARE: FRASESQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11
                                                                                                                                                                                                                                                                                   ; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
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                                                                                                                                                                                    Best Local Similarity 95.0
Matches 19; Conservative
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Best Local Similarity 95.0
Matches 19; Conservative
                                             LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
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US-10-821-234-1234
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US-11-186-422-12
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LENGTH: 215
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US-11-087-099-4976
Sequence 4976, Application US/11087099
Sequence 4976, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 4976
LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75; DB 7; Length 141;
Pred. No. 6.3e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75; DB 7; Length 142; Pred. No. 6.3e-05; 1; Mismatches 4; Indels
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Sequence 313, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATUCO:
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
FILLE OF INVENTION: Genea and Uses for Plant Improvement
FILE REPERBENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
NUMBER OF FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 313
                                                                                                                                                                          Sequence 9185, Application US/11087099
Sequence 9185, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genea and Uses for Plant Improvement
FILE REPERBACE: 38-21(53450) B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9185
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1; Mismatches
                                                                         41 KDPNKPKRPPSAFFVFMEE 59
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                                             2 KDPNAPKRLPSAFFLFCSE 20
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Best Local Similarity 73.7%;
Matches 14; Conservative
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Best Local Similarity 73.7%;
Matches 14; Conservative
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US-11-087-099-9185
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US-11-087-099-4976
14; Conservative
Matches
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US-11-087-099-1105
; Sequence 1105, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 141;
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Pred. No. 3.4e-05;
                                                                                Sequence 30.3. Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERENCE: 38-21(53450) B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3073
LENGTH: 141
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPREBRUCE: 38-21(53450) B EP
CURRENT APPLICATION WURBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                71.8%; Score 79; DB 7; I
ilarity 78.9%; Pred. No. 1.4e-05;
Conservative 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Hordeum vulgare subsp. vulgare US-11-087-099-1105
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; ORGANISM: Narcissus pseudonarcissus
US-11-087-099-7075
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Best Local Similarity 73.7%;
Matches 14; Conservative
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73.7%;
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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                                                               US-11-087-099-3073
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US-11-087-099-3073
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TYPE: PRT ORGANISM:

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Query Match 68.2%; Score 75; DB 7; Length 152; Best Local Similarity 73.7%; Pred. No. 6.7e-05; Matches 14; Conservative 1; Mismatches 4; Indels
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
ITLE OF INVENTION: Genes and Uses for Plant Improvement
FIRE REFERENCE: 32-21(55450) B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3510
LENGTH: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1). (152)
OTHER INFORMATION: Public GI no. 18645
Sequence 1566, Application US/11172740 Publication No. US20060057724A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
TYPE:
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
'~~**TON: (1)...(152)
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NAME/KEY: misc_feature
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                             RESULT 13
US-11-172-740-1565
i Sequence 1565, Application US/11172740
i Publication No. US20060057724A1
i GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROV, Nickolai
APPLICANTON NUMBER: US/11/172,740
CURRENT APPLICATION NUMBER: 60/584,829
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 1565
LENGTH: 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
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                                                                       Score 75; DB 7; Length 152; Pred. No. 6.7e-05; 1; Mismatches 4; Indels
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OTHER INFORMATION: Ceres CLONE ID no. 721511
                                                                                                                                                                           2 KDPNAPKRLPSAFFLFCSE 20
                                                                                                                                                                                                           39 KDPNKPKRPPSAFFVFMEE 57
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                                                                       Query Match
Best Local Similarity 73.7%;
Matches 14; Conservative
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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, ORGANISM: Glycine max
US-11-087-099-313
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US-11-172-740-1566
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GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: BROWER, Vyacheelav
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE REFERENCE: 2750-1602PUS2
CURRENT APPLICATION NUMBER: US/11/172,740
PRIOR FILING DATE: 2004-06-30
PRIOR PLING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 1566
LENGTH: 152
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OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
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; ORGANISM: Vicia faba
US-11-087-099-3510
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Query Match 66.4%; Score 73; DB 7; Length 149;
Best Local Similarity 68.4%; Pred. No. 0.00014;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps
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